

From: Bunner, Bridget
Sent: Wednesday, May 11, 2005 9:43 AM
To: STIC-Biotech/ChemLib
Subject: sequence search request

Hi! I'd like to request a sequence search for case 10/649,952:

1. the amino acid sequence of SEQ ID NO: 2
2. the amino acid sequence encoded by SEQ ID NO: 1

Thanks!

Bridget Bunner

Art Unit 1647
Rem 4C65
(571) 272-0881
mailbox 4C70

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2-_____
Date Searcher Picked up: _____
Date Completed: 5/13
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA#: _____ AA#: _____
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

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Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 13, 2005, 09:41:10 ; Search time 134 Seconds
(without alignments)
413.825 Million cell updates/sec

Title: US-10-649-952A-1

Perfect score: 846

Sequence: 1 MASGVASDGVIKFNDMKV.....CTLAELGGSVISLEGKPL 166

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1432185 seqs, 334051727 residues

Total number of hits satisfying chosen parameters: 1432185

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*

- 1: /cgn2_6/prodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/prodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/prodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/prodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/prodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/prodata/2/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/prodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/prodata/2/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/prodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/prodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/prodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/prodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/prodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/prodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/prodata/2/pubpaa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/prodata/2/pubpaa/US10_NEW_PUB.pep:*
- 18: /cgn2_6/prodata/2/pubpaa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/prodata/2/pubpaa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/prodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	846	100.0	166	16	US-10-649-952A-1
2	764	90.3	149	16	US-10-408-765A-2270
3	702	83.0	166	14	US-10-205-342-21
4	699	82.6	166	14	US-10-205-823-72
5	699	82.6	166	16	US-10-408-765A-1910
6	699	82.6	205	15	US-10-158-034-93
7	557.5	65.9	148	16	US-10-408-765A-2351
8	460	54.4	129	15	US-10-158-034-94
9	450	53.2	156	15	US-10-158-034-68
10	273	32.3	106	15	US-10-264-049-4340
11	267.5	31.6	143	15	US-10-369-493-2293
12	253.5	30.0	141	16	US-10-263-255-2
13	245.5	29.0	141	16	US-10-263-255-4

14	239.5	28.3	139	15	US-10-424-599-186070	Sequence 186070,
15	230	27.2	60	14	US-10-029-386-30107	Sequence 30107, A
16	230	27.2	190	15	US-10-369-493-2272	Sequence 2272, Ap
17	227	26.8	145	15	US-10-425-114-37040	Sequence 37040, A
18	227	26.8	161	15	US-10-425-114-59591	Sequence 59591, A
19	227	26.8	171	15	US-10-425-114-39098	Sequence 39098, A
20	227	26.8	179	15	US-10-425-114-38879	Sequence 38879, A
21	227	26.8	179	15	US-10-425-114-41223	Sequence 41223, A
22	227	26.8	179	15	US-10-425-114-44883	Sequence 44883, A
23	227	26.8	179	15	US-10-425-114-51312	Sequence 51312, A
24	227	26.8	179	15	US-10-425-114-57582	Sequence 57582, A
25	227	26.8	179	15	US-10-425-114-59194	Sequence 59194, A
26	227	26.8	179	15	US-10-425-114-59883	Sequence 59883, A
27	227	26.8	179	15	US-10-425-114-66714	Sequence 66714, A
28	227	26.8	179	15	US-10-425-114-67765	Sequence 67765, A
29	227	26.8	179	15	US-10-425-114-72052	Sequence 72052, A
30	227	26.8	179	15	US-10-425-114-72097	Sequence 72097, A
31	224.5	26.5	139	16	US-10-767-701-45854	Sequence 45854, A
32	223.5	26.4	194	16	US-10-767-701-43979	Sequence 43979, A
33	221	26.1	139	15	US-10-250-613-9	Sequence 9, Appl
34	221	26.1	157	15	US-10-425-114-59062	Sequence 59062, A
35	221	26.1	173	15	US-10-425-114-66010	Sequence 66010, A
36	221	26.1	176	15	US-10-425-114-69864	Sequence 69864, A
37	221	26.1	177	15	US-10-425-114-44953	Sequence 44953, A
38	221	26.1	177	15	US-10-425-114-48026	Sequence 48026, A
39	221	26.1	177	15	US-10-425-114-48329	Sequence 48329, A
40	221	26.1	177	15	US-10-425-114-49519	Sequence 49519, A
41	221	26.1	177	15	US-10-425-114-53265	Sequence 53265, A
42	221	26.1	177	15	US-10-425-114-53325	Sequence 53325, A
43	221	26.1	177	15	US-10-425-114-66577	Sequence 66577, A
44	221	26.1	177	15	US-10-425-114-66602	Sequence 66602, A
45	221	26.1	181	15	US-10-425-114-69951	Sequence 69951, A

ALIGNMENTS

RESULT 1

US-10-649-952A-1
; Sequence 1, Application US/10649952A
; Publication No. US20040157326A1
; GENERAL INFORMATION:
; APPLICANT: DAIICHI SUNTORY PHARMA CO., LTD.
; APPLICANT: Daiichi Suntory Biomedical Research Ltd.
; APPLICANT: Miura, Kenju
; APPLICANT: Haruyama, Munetada
; APPLICANT: Kodama, Shiko
; TITLE OF INVENTION: Promoters of the growth and/or differentiation of hematopoietic stem cells and/or hematopoietic progenitors
; FILE OF INVENTION: 58777.000013
; FILE REFERENCE: 58777.000013
; CURRENT APPLICATION NUMBER: US/10/649,952A
; CURRENT FILING DATE: 2003-08-28
; PRIOR APPLICATION NUMBER: PCT/JPO2/13862
; PRIOR FILING DATE: 2002-12-27
; PRIOR APPLICATION NUMBER: JAPAN 400330/2001
; PRIOR FILING DATE: 2001-12-28
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Human
US-10-649-952A-1

Query Match 100.0%; Score 846; DB 16; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.3e-76;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASGVASDGVTKFNDMKVKRKSSTPEEVKKRKAVALFCLSEDKKNIILEEGKEILVGV 60

Db 1 MASGVASDGVTKFNDMKVKRKSSTPEEVKKRKAVALFCLSEDKKNIILEEGKEILVGV 60

QY 61 GQVDDPVATFVKMLPKDKDCRYALDYATYETKESKKEDLVFIWFAPESAPLKSMMIYASS 120

Db 61 GQTVDDPYATFVKMLPKDCKRYALYDQYETKESKEDLVFIWAPESAPLKSMIYASS 120
 Qy 121 KDAIKKKLTGKHELOQANCYEEVKDRCTLAELKGGSAVISLEGKPL 166
 Db 121 KDAIKKKLTGKHELOQANCYEEVKDRCTLAELKGGSAVISLEGKPL 166

RESULT 2

US-10-408-765A-2270
 ; Sequence 2270, Application US/10408765A
 ; Publication No. US20040101874A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ghosh, Soumitra S.
 ; APPLICANT: Faby, Eoin D.
 ; APPLICANT: Zhang, Bing
 ; APPLICANT: Gibson, Bradford W.
 ; APPLICANT: Taylor, Steven W.
 ; APPLICANT: Glenn, Gary M.
 ; APPLICANT: Warnock, Dale E.
 ; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
 ; FILE REFERENCE: 660088.465
 ; CURRENT APPLICATION NUMBER: US/10/408.765A
 ; CURRENT FILING DATE: 2003-04-04
 ; NUMBER OF SEQ ID NOS: 3077
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2270
 ; LENGTH: 149
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-408-765A-2270

Query Match 90.3%; Score 764; DB 16; Length 149;
 Best Local Similarity 100.0%; Pred. No. 1.9e-68;
 Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 18 MKVKRSTPPEVKRKKAVLCFSEDKNKILLEGKILVGDVGQTVDDPYATFVKMLPD 77
 Db 1 MKVKRSTPPEVKRKKAVLCFSEDKNKILLEGKILVGDVGQTVDDPYATFVKMLPD 60
 Qy 78 KDCRYALYDQYETKESKEDLVFIWAPESAPLKSMIYASSKDAIKKKLTGKHELOA 137
 Db 61 KDCRYALYDQYETKESKEDLVFIWAPESAPLKSMIYASSKDAIKKKLTGKHELOA 120
 Qy 138 NCYEEVKDRCTLAELKGGSAVISLEGKPL 166
 Db 121 NCYEEVKDRCTLAELKGGSAVISLEGKPL 149

RESULT 3

US-10-205-342-21
 ; Sequence 21, Application US/10205342
 ; Publication No. US20030108906A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Warner-Lambert Company
 ; APPLICANT: Lee, Kevin
 ; APPLICANT: Dixon, Alistair
 ; APPLICANT: Brookesbank, Robert
 ; APPLICANT: Pinnock, Robert
 ; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
 ; FILE REFERENCE: WL-A-018198
 ; CURRENT APPLICATION NUMBER: US/10/205.342
 ; CURRENT FILING DATE: 2002-07-24
 ; PRIOR APPLICATION NUMBER: GB 0118354.0
 ; PRIOR FILING DATE: 2001-07-27
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 21
 ; LENGTH: 166
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 ; FEATURE:

; OTHER INFORMATION: Protein: Cofilin
 US-10-205-342-21
 Query Match 83.0%; Score 702; DB 14; Length 166;
 Best Local Similarity 81.3%; Pred. No. 3.5e-62;
 Matches 135; Conservative 14; Mismatches 17; Indels 0; Gaps 0;
 Qy 1 MASGAVSDGVIKVFNDMKVKRSTPPEVKRKKAVLCFSEDKNKILLEGKILVGDV 60
 Db 1 MASGVTVNDDEVIKVFNDMKVKRSTQEEIKRKKAVLCFSLDDKQRIIVEAKQILVGI 60
 Qy 61 GQTVDDPYATFVKMLPKDCKRYALYDQYETKESKEDLVFIWAPESAPLKSMIYASS 120
 Db 61 GDTVEDPYTSFVKLLPLNDCKRYALYDQYETKESKEDLVFIWAPESAPLKSMIYASS 120
 Qy 121 KDAIKKKLTGKHELOQANCYEEVKDRCTLAELKGGSAVISLEGKPL 166
 Db 121 KDAIKKKFTGIRHEWQVNGLLDDIKDRSTLGEKLGSSVVVSLEGKPL 166

RESULT 4

US-10-205-823-72
 ; Sequence 72, Application US/10205823
 ; Publication No. US20030108963A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schlegel, Robert
 ; APPLICANT: Monahan, John E.
 ; APPLICANT: Endege, Wilson O.
 ; APPLICANT: Gannavarapu, Manjula
 ; APPLICANT: Gorbacheva, Bella
 ; APPLICANT: Hoersch, Sebastian
 ; APPLICANT: Kamatkar, Shubhangi
 ; APPLICANT: Monsey, Angela M.
 ; APPLICANT: Glatt, Karen
 ; APPLICANT: Zhao, Xumei
 ; APPLICANT: Anderson, Dustin
 ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
 ; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
 ; FILE REFERENCE: MRI-044
 ; CURRENT APPLICATION NUMBER: US/10/205.823
 ; CURRENT FILING DATE: 2002-07-25
 ; PRIOR APPLICATION NUMBER: 60/307,982
 ; PRIOR FILING DATE: 2001-07-25
 ; PRIOR APPLICATION NUMBER: 60/314,356
 ; PRIOR FILING DATE: 2001-08-22
 ; PRIOR APPLICATION NUMBER: 60/325,020
 ; PRIOR FILING DATE: 2001-09-25
 ; PRIOR APPLICATION NUMBER: 60/341,746
 ; PRIOR FILING DATE: 2001-12-12
 ; PRIOR APPLICATION NUMBER: 60/362,158
 ; PRIOR FILING DATE: 2002-03-05
 ; NUMBER OF SEQ ID NOS: 455
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 72
 ; LENGTH: 166
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-205-823-72

Query Match 82.6%; Score 699; DB 14; Length 166;
 Best Local Similarity 80.7%; Pred. No. 7.1e-62;
 Matches 134; Conservative 15; Mismatches 17; Indels 0; Gaps 0;
 Qy 1 MASGAVSDGVIKVFNDMKVKRSTPPEVKRKKAVLCFSEDKNKILLEGKILVGDV 60
 Db 1 MASGVTVNDDEVIKVFNDMKVKRSTQEEIKRKKAVLCFSLDDKQRIIVEAKQILVGI 60
 Qy 61 GQTVDDPYATFVKMLPKDCKRYALYDQYETKESKEDLVFIWAPESAPLKSMIYASS 120
 Db 61 GDTVEDPYTSFVKLLPLNDCKRYALYDQYETKESKEDLVFIWAPESAPLKSMIYASS 120
 Qy 121 KDAIKKKLTGKHELOQANCYEEVKDRCTLAELKGGSAVISLEGKPL 166

Db 121 KDAIKKKFTGKHEWQVNGLLDKDRSTLGEKLGKGNVVSLEKPL 166

RESULT 5
US-10-408-765A-1910
; Sequence 1910, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1910
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1910

Query Match 82.6%; Score 699; DB 16; Length 166;
Best Local Similarity 80.7%; Pred. No. 7.le-62;
Matches 134; Conservative 15; Mismatches 17; Indels 0; Gaps 0;
QY 1 MASGVAVSGVIVKVFNDMKVRKSTPEEVKRRKAVLFCLSDDKNNIILEEGKEILVGDV 60
DB 1 MASGVTVDNVIKVFNDMKVRKSTPEEVKRRKAVLFCLSDDKNNIILEEGKEILVGDV 60
QY 61 GOTVDDPYATFVKMLPDKCRYALYDATYETKESKEDLVFIFWAPESAPLKSMMIYASS 120
DB 61 GOTVEDPYTSFVKLLPLNDCRYALYDATYETKESKEDLVFIFWAPESAPLKSMMIYASS 120
QY 121 KDAIKKKFTGKHEWQVNGLLDKDRSTLGEKLGKGNVVSLEKPL 166
DB 121 KDAIKKKFTGKHEWQVNGLLDKDRSTLGEKLGKGNVVSLEKPL 166

RESULT 6
US-10-158-034-93
; Sequence 93, Application US/10158034
; Publication No. US20030219758A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ10C1
; CURRENT APPLICATION NUMBER: US/10/158,034
; CURRENT FILING DATE: 2002-05-31
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 93
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-158-034-93

Query Match 82.6%; Score 699; DB 15; Length 205;
Best Local Similarity 80.7%; Pred. No. 9.4e-62;
Matches 134; Conservative 15; Mismatches 17; Indels 0; Gaps 0;
QY 1 MASGVAVSGVIVKVFNDMKVRKSTPEEVKRRKAVLFCLSDDKNNIILEEGKEILVGDV 60
DB 40 MASGVTVDNVIKVFNDMKVRKSTPEEVKRRKAVLFCLSDDKNNIILEEGKEILVGDV 99

QY 61 GOTVDDPYATFVKMLPDKCRYALYDATYETKESKEDLVFIFWAPESAPLKSMMIYASS 120
DB 100 GOTVEDPYTSFVKLLPLNDCRYALYDATYETKESKEDLVFIFWAPESAPLKSMMIYASS 159
QY 121 KDAIKKKFTGKHEWQVNGLLDKDRSTLGEKLGKGNVVSLEKPL 166
DB 160 KDAIKKKFTGKHEWQVNGLLDKDRSTLGEKLGKGNVVSLEKPL 205

RESULT 7
US-10-408-765A-2351
; Sequence 2351, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2351
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-2351

Query Match 65.9%; Score 557.5; DB 16; Length 148;
Best Local Similarity 72.5%; Pred. No. 9e-48;
Matches 108; Conservative 18; Mismatches 22; Indels 1; Gaps 1;
QY 18 MKVRKSTPEEVKRRKAVLFCLSDDKNNIILEEGKEILVGDVGTVDPYATFVKMLPD 77
DB 1 MKVRKSTPEEVKRRKAVLFCLSDDKNNIILEEGKEILVGDVGTVDPYATFVKMLPD 60
QY 78 KDCRYALYDATYETKESKEDLVFIFWAPESAPLKSMMIYASSKDAIKKKFTGKHEWQV 137
DB 61 KDCRYALYDASPEVKRKEELMFLWAPELAPLKSMMIYASSKDAIKKKFTGKHEWQV 120
QY 138 NCYEEVKDRCTLAELKGGSAVISLEKPL 166
DB 121 NGPEDLNRACTAEKLGGLIIVAFEGCPV 148

RESULT 8
US-10-158-034-94
; Sequence 94, Application US/10158034
; Publication No. US20030219758A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ10C1
; CURRENT APPLICATION NUMBER: US/10/158,034
; CURRENT FILING DATE: 2002-05-31
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 94
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-158-034-94

Query Match 82.6%; Score 699; DB 15; Length 205;
Best Local Similarity 80.7%; Pred. No. 9.4e-62;
Matches 134; Conservative 15; Mismatches 17; Indels 0; Gaps 0;
QY 1 MASGVAVSGVIVKVFNDMKVRKSTPEEVKRRKAVLFCLSDDKNNIILEEGKEILVGDV 60
DB 40 MASGVTVDNVIKVFNDMKVRKSTPEEVKRRKAVLFCLSDDKNNIILEEGKEILVGDV 99

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; NAME/KEY: misc feature
; LOCATION: (123)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (126)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (127)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (128)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-158-034-94

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Query Match 54.4%; Score 460; DB 15; Length 129;
Best Local Similarity 81.3%; Pred. No. 4.4e-38;
Matches 87; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

Qy 1 MASGVAVSDGVKVFNDKVRKSTPEEVKKRKAVALFCLSDKKNILLEGKEILVGDV 60
Db 13 MASGVTNDEVKVFNDKVRKSTQBEIKRKAVALFCLSDKKNILLEGKEILVGDV 72
Qy 61 GQTVDDPYATFVKMLPDKCRYALYDATYETKESKEDLVFIWAPESAPL 107
Db 73 GDTVEDPYTSFVKLLPLNDKCRYALYDATYETKESKEDLVFIWAPESAPL 119

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RESULT 9
US-10-158-034-68
; Sequence 68, Application US/10158034
; Publication No. US20030219758A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ10C1
; CURRENT APPLICATION NUMBER: US/10/158,034
; CURRENT FILING DATE: 2002-05-31
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 68
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-158-034-68

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Query Match 53.2%; Score 450; DB 15; Length 156;
Best Local Similarity 81.7%; Pred. No. 5.7e-37;
Matches 85; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MASGVAVSDGVKVFNDKVRKSTPEEVKKRKAVALFCLSDKKNILLEGKEILVGDV 60
Db 45 MASGVTNDEVKVFNDKVRKSTQBEIKRKAVALFCLSDKKNILLEGKEILVGDV 104
Qy 61 GQTVDDPYATFVKMLPDKCRYALYDATYETKESKEDLVFIWAPESAPL 104
Db 105 GDTVEDPYTSFVKLLPLNDKCRYALYDATYETKESKEDLVFIWAPESAPL 148

```

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RESULT 10
US-10-264-049-4340
; Sequence 4340, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133P1
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569

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; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: Patent In Ver. 3.1
; SEQ ID NO 4340
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (91)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (100)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-049-4340

```

```

Query Match 32.1%; Score 273; DB 15; Length 106;
Best Local Similarity 55.2%; Pred. No. 1.8e-19;
Matches 58; Conservative 13; Mismatches 34; Indels 0; Gaps 0;

Qy 8 SDGVKVFNDKVRKSTPEEVKKRKAVALFCLSDKKNILLEGKEILVGDVQVDDP 67
Db 1 ADEVCRIFYDMKVRKSTPEEVKKRKAVALFCLSDKKNILLEGKEILVGDVQVDDP 60
Qy 68 YATFVKMLPDKCRYALYDATYETKESKEDLVFIWAPESAPL 112
Db 61 FKHFVGMLLKKIVAMLCMQALQKQSEKKLMPFWGAPXLTGFK 105

```

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RESULT 11
US-10-369-493-22293
; Sequence 22293, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 22293
; LENGTH: 143
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-369-493-22293

```

```

Query Match 31.6%; Score 267.5; DB 15; Length 143;
Best Local Similarity 37.8%; Pred. No. 9.6e-19;
Matches 54; Conservative 31; Mismatches 37; Indels 21; Gaps 3;

Qy 3 SGVAVSDGVKVFNDKVRKSTPEEVKKRKAVALFCLSDKKNILLEGKEILVGDV 62
Db 4 SGVAVSDGVKVFNDKVRKSTPEEVKKRKAVALFCLSDKKNILLEGKEILVGDV 44
Qy 63 TVDDPYATFVKMLPDKCRYALYDATYETKESKEDLVFIWAPESAPLKSMTYASS 120
Db 45 STDPYDAFLEKLPENDCLYALYDFEYINGEKGSKIVFTWSPDTAPVRSKMYASS 104
Qy 121 KDAIKKLTGKIKHELQANCYEEV 143
Db 105 KDALRRALNGVSTDVQGTDFSEV 127

```

```
RESULT 12
US-10-263-255-2
; Sequence 2, Application US/10263255
; Publication No. US20040191771A1
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; APPLICANT: Chua, Penelope
; APPLICANT: Nislow, Corey
; TITLE OF INVENTION: Candida Albicans Cofilin
; FILE REFERENCE: CYTOPO72
; CURRENT APPLICATION NUMBER: US/10/263,255
; CURRENT FILING DATE: 2002-10-01
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Candida Albicans
US-10-263-255-2
Query Match      30.0%; Score 253.5; DB 16; Length 141;
Best Local Similarity 33.6%; Pred. No. 2.4e-17;
Matches 48; Conservative 38; Mismatches 36; Indels 21; Gaps 3;

QY 3 SGVAVSDGVKVFNDMKVRKSTPPEVKRKKAVLFCLSDEKKNIILEGKEILVGDVGQ 62
DB 4 SGTVADESILTAFLDLK-----LGRKYKVFIFLNDKTKQIVVEQ-----T 44

QY 63 TVDDPVATFVKMLPDKDCRYALYDATYET--KESKKEDLVFIFWAPESAPLKSMMIYASS 120
DB 45 STEQEYDAFLEKLPENECRYAVDYFDYDYGGEGRKSKIVFTWSPDTPAPVRKMWYASS 104

QY 121 KDAIKKKLTGKIKHELQANCYEEV 143
DB 105 KDSLREALNGVAADVQGTDFSEV 127

RESULT 13
US-10-263-255-4
; Sequence 4, Application US/10263255
; Publication No. US20040191771A1
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; APPLICANT: Chua, Penelope
; APPLICANT: Nislow, Corey
; TITLE OF INVENTION: Candida Albicans Cofilin
; FILE REFERENCE: CYTOPO72
; CURRENT APPLICATION NUMBER: US/10/263,255
; CURRENT FILING DATE: 2002-10-01
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Candida albicans
US-10-263-255-4
Query Match      29.0%; Score 245.5; DB 16; Length 141;
Best Local Similarity 33.6%; Pred. No. 1.5e-16;
Matches 48; Conservative 37; Mismatches 37; Indels 21; Gaps 3;

QY 3 SGVAVSDGVKVFNDMKVRKSTPPEVKRKKAVLFCLSDEKKNIILEGKEILVGDVGQ 62
DB 4 SGTVADESILTAFLDLK-----LGRKYKVFIFLNDKTKQIVVEQ-----T 44

QY 63 TVDDPVATFVKMLPDKDCRYALYDATYET--KESKKEDLVFIFWAPESAPLKSMMIYASS 120
DB 45 STEQEYDAFLEKLPENECRYAVDYFDYDYGGEGRKSKIVFTWSPDTPAPVRKMWYASS 104

QY 121 KDAIKKKLTGKIKHELQANCYEEV 143
DB 105 KDSLREALNGVAADVQGTDFSEV 127
```

```
RESULT 14
US-10-424-599-186070
; Sequence 186070, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(S3223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 186070
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_139033C.1.pap
US-10-424-599-186070
Query Match      28.3%; Score 239.5; DB 15; Length 139;
Best Local Similarity 34.9%; Pred. No. 5.9e-16;
Matches 52; Conservative 27; Mismatches 51; Indels 19; Gaps 3;

QY 3 SGVAVSDGVKVFNDMKVRKSTPPEVKRKKAVLFCLSDEKKNIILEGKEILVGDVGQ 62
DB 4 TGIADVNECVNEFNAPKLRNT-----HRYIVF-----KIENAKEIKIEKKGE 45

QY 63 TVDDPVATFVKMLPDKDCRYALYDATYETKESKKEDLVFIFWAPESAPLKSMMIYASSKD 122
DB 46 TTAS-YDFELKQLPNDCHYAVYNEYNQADGFRSKIVFLWAPDTAPTKSKMLYACTKD 104

QY 123 AIKKKLTGKIKHELQANCYEEVKDRCTLAEE 151
DB 105 TLKKNLQGLQVEMQGTDKSEVDQSEVLAK 133

RESULT 15
US-10-029-386-30107
; Sequence 30107, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 30107
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL132765.16
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.3
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.6
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 9.9
; OTHER INFORMATION: SWISSPROT HIT: P18282, EVALUUE 1.00e-29
US-10-029-386-30107
Query Match      27.2%; Score 230; DB 14; Length 60;
Best Local Similarity 74.1%; Pred. No. 1.7e-15;
Matches 43; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

QY 44 KKNIILEGKEILVGDVGQTVDDPVATFVKMLPDKDCRYALYDATYETKESKKEDLVF 101
```

Db 1 KKCIIVEEGKEILVGDVGWTTITDPFKHFVGMPLPEKDCRYALYDASFETKESRKEELMF 58

Search completed: May 13, 2005, 09:50:41
Job time : 135 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 13, 2005, 09:28:54 ; Search time 161 Seconds
(without alignments)
398.772 Million cell updates/sec

Title: US-10-649-952A-1
Perfect score: 846
Sequence: 1 MASGVAVSDGVKVFNDMKV.....CTLAEKLGGSAVISLEGKPL 166

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001s:*
- 5: Geneseq2002s:*
- 6: Geneseq2003as:*
- 7: Geneseq2003bs:*
- 8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	846	100.0	166	5	ABB81882 Human cof
2	846	100.0	166	6	ADA37012 Human cof
3	846	100.0	166	8	ADI24535 Human mod
4	846	100.0	166	8	ADO05889 Human cof
5	846	100.0	166	8	ADO30534 Pancreas
6	846	100.0	229	8	ADQ65133 Novel hum
7	842	99.5	187	6	ABR41637 Human DIT
8	841	99.4	239	8	ADN99790 Novel hum
9	764	90.3	149	7	ADJ70464 Human hea
10	702	83.0	166	6	ABR41956 Mouse cof
11	699	82.6	166	4	AAM78545 Human pro
12	699	82.6	166	7	ADB75248 Prostata
13	699	82.6	166	7	ADJ70104 Human hea
14	699	82.6	166	8	ADI24536 Human mod
15	699	82.6	205	4	AAU18546 Human cyt
16	699	82.6	207	4	AAM79529 Human pro
17	666.5	78.8	154	8	ADN99460 Novel hum
18	645.5	76.3	153	8	ADN99430 Novel hum
19	616	72.8	127	3	AAG03978 Human sec
20	606.5	71.7	165	3	AAG03876 Human sec
21	606.5	71.7	165	4	AAM40267 Human pol
22	606.5	71.7	165	8	ADI24537 Human mod
23	606.5	71.7	165	8	ADQ30570 Pancreas
24	606.5	71.7	165	8	ADP23096 PRO polyp
25	606.5	71.7	188	4	AAM42053 Human pol

ALIGNMENTS

RESULT 1
ABB81882
ID ABB81882 standard; protein; 166 AA.
AC ABB81882;
XX
XX
DT 23-SEP-2002 (first entry)
XX
DE Human cofilin 1 (non-muscle).
XX
XX
KW Human; cofilin 1; CFL1; gene therapy; antisense gene therapy;
immunological disorder.
XX
XX Homo sapiens.
XX
XX WO200194376-A1.
XX
XX
PD 13-DEC-2001.
XX
XX
PF 11-JUN-2001; 2001WO-US018815.
XX
XX
PR 09-JUN-2000; 2000US-0210884P.
XX
XX (GENA-) GENAISSANCE PHARM INC.
XX
XX Anastasio AE, Duda A, Klieem SE, Koshy B, Sausker EA;
XX
XX WPI: 2002-566437/60.
XX
XX N-PSDB; ABO88640, ABO88641.
XX
XX Novel genetic variants of human cofilin 1, CFL1 gene for studying
expression, function of the gene and expressing CFL1 protein useful in
identifying drugs to treat immunological disorders.
XX
XX Disclosure; Fig 3; 84pp; English.

The invention relates to a novel polynucleotide sequence which is a polymorphic variant of a reference sequence for the cofilin 1 (non-muscle) (CFL1) gene or its fragment, or a polymorphic variant of a reference sequence for a CFL1 cDNA or its fragment. The polynucleotide of the invention may have a use in gene therapy, and in antisense gene therapy. The polynucleotide is useful for studying the expression and function of CFL1 and expressing CFL1 protein for use in screening for candidate drugs to treat diseases related to CFL1 activity. The polymorphism and haplotype data are useful for validating whether CFL1 is a suitable target for drugs to treat immunological disorders, screening for such drugs and reducing bias in clinical trials of such drugs. The present sequence represents the human cofilin 1 (non-muscle) of the

26 566.5 67.0 170 8 ADI24538 Human mod
27 557.5 65.9 148 7 ADJ70545 Human hea
28 520.5 61.5 111 7 ADE15627 Human str
29 460 54.4 129 4 AAU18547 Human cyt
30 450 53.2 156 4 AAU18521 Human cyt
31 426 50.4 144 8 ADI24541 Human mod
32 402.5 47.6 131 8 ADF30110 Human sec
33 401.5 47.5 136 8 ADI24540 Human mod
34 390 46.1 110 8 ADN99316 Novel hum
35 390 46.1 110 8 ADP30004 Human sec
36 386 45.6 180 8 ADI24539 Human mod
37 374 44.2 209 4 AEG20129 Novel hum
38 354 41.8 86 3 AAG01408 Human sec
39 287 33.9 69 3 AAG01407 Human sec
40 273 32.3 106 5 ABE43208 Human ova
41 267.5 31.6 143 8 ADS43863 Bacterial
42 253.5 30.0 141 8 ADN12253 C. albica
43 245.5 29.0 141 8 ADN12255 C. albica
44 230 27.2 60 8 ABO56473 Human gen
45 230 27.2 190 8 ADN19619 Bacterial

CC invention
XX
SQ Sequence 166 AA;
Query Match 100.0%; Score 846; DB 5; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.4e-83;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MASGVAVSDGVIVFNDKVRKSTPEEVKKRKAVALFCLSEDKKNIIIEGKEILVGDV 60
Db 1 MASGVAVSDGVIVFNDKVRKSTPEEVKKRKAVALFCLSEDKKNIIIEGKEILVGDV 60
Qy 61 GQTVDDPYATFVKMLPKDCRYALYDATYETKESKEDLVFIWAPESAPLKSMMIYASS 120
Db 61 GQTVDDPYATFVKMLPKDCRYALYDATYETKESKEDLVFIWAPESAPLKSMMIYASS 120
Qy 121 KDAIKKKLTGIKHELOQANCYEEVKDRCTLAELGSSAVISLEGKPL 166
Db 121 KDAIKKKLTGIKHELOQANCYEEVKDRCTLAELGSSAVISLEGKPL 166
RESULT 2
ADA37012
ID ADA37012 standard; protein; 166 AA.
XX
AC ADA37012;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human cofillin protein SEQ ID NO:1.
XX
KW proliferation; differentiation; haematopoietic stem cell; cofillin;
KW vasotropic; antianaemic; cytostatic; vulnerable; nephrotropic;
KW hepatotropic; haematopoietic hypofunction; Fanconi's disease;
KW malignant lymphoma; acute leukaemia; chronic hepatic obstruction;
KW kidney failure; surgical trauma; transfusion trauma; infection;
KW snakebite; haemorrhagic uraemia; splenomegaly; Bernard-Soulier disease;
KW Glanzmann's thrombasthenia; idiopathic thrombocytopenic purpura; human.
XX
OS Homo sapiens.
XX
FN WO2003057241-A1.
XX
PD 17-JUL-2003.
XX
PF 27-DEC-2002; 2002WO-JP013862.
XX
PR 28-DEC-2001; 2001JP-00400330.
XX
PA (DAII-) DAIICHI SUNTORY PHARMA CO LTD.
PA (SUNR) SUNTORY LTD.
PA (DAII-) DAIICHI SUNTORY BIOMEDICAL RES LTD.
XX
PI Miura K, Haruyama M, Kodama S;
XX
DR WPI; 2003-587077/55.
DR N-PSDB; ADA37013.
XX
PT Agents containing cofillin promoting proliferation and differentiation of
PT haematopoietic stem cells and their precursors for treatment of
PT haematopoietic deficiency diseases.
XX
FS Claim 2; Fig 1; 57pp; Japanese.
XX
CC The present invention describes agents (A) promoting the proliferation
CC and/or differentiation of haematopoietic stem cells and/or their
CC precursor cells. (A) contain cofillin or a peptide of similar activity as
CC active component. Also described: (1) promoting the proliferation and/or
CC differentiation of haematopoietic stem cells and/or their precursor
CC cells, using (A); and (2) treating diseases associated with
CC haematopoietic cell deficiency, using (A). (A) have vasotropic,
CC antianaemic, cytostatic, vulnerable, nephrotropic and hepatotropic
CC activities. (A) can be used for treating and preventing diseases

CC associated with a diffuse decrease in haematopoietic cell numbers and/or
CC haematopoietic hypofunction, such as Fanconi's disease, malignant
CC lymphoma, acute leukaemia, chronic hepatic obstruction, kidney failure,
CC surgical or transfusion trauma, serious infections, snakebite,
CC haemorrhagic uraemia, splenomegaly, Bernard-Soulier disease, Glanzmann's
CC thrombasthenia, and idiopathic thrombocytopenic purpura. The present
CC sequence represents human cofillin, which is given in the exemplification
CC of the present invention.
XX
SQ Sequence 166 AA;
Query Match 100.0%; Score 846; DB 6; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.4e-83;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MASGVAVSDGVIVFNDKVRKSTPEEVKKRKAVALFCLSEDKKNIIIEGKEILVGDV 60
Db 1 MASGVAVSDGVIVFNDKVRKSTPEEVKKRKAVALFCLSEDKKNIIIEGKEILVGDV 60
Qy 61 GQTVDDPYATFVKMLPKDCRYALYDATYETKESKEDLVFIWAPESAPLKSMMIYASS 120
Db 61 GQTVDDPYATFVKMLPKDCRYALYDATYETKESKEDLVFIWAPESAPLKSMMIYASS 120
Qy 121 KDAIKKKLTGIKHELOQANCYEEVKDRCTLAELGSSAVISLEGKPL 166
Db 121 KDAIKKKLTGIKHELOQANCYEEVKDRCTLAELGSSAVISLEGKPL 166
RESULT 3
ADI24535
ID ADI24535 standard; protein; 166 AA.
XX
AC ADI24535;
XX
DT 15-APR-2004 (first entry)
XX
DE Human modifier of Chk1 (MCHK) protein SEQ ID NO:85.
XX
KW Chk1 pathway modulating agent; modifier of Chk1; MCHK; cytostatic;
KW gene therapy; cancer; human.
XX
OS Homo sapiens.
XX
FN WO2004004785-A1.
XX
PD 15-JAN-2004.
XX
PF 09-JUL-2003; 2003WO-US021379.
XX
PR 10-JUL-2002; 2002US-0394845P.
PR 16-SEP-2002; 2002US-0410986P.
XX
PA (EXEL-) EXELIXIS INC.
XX
PI Francis-Lang H, Roche S, Joo DM, Nicoll M, Hai B, Zhang H;
PI Lickteig K, Amundsen CD, Jin Y, Adamkewicz JI, Platt DM;
PI Hammonds RG;
XX
DR WPI; 2004-083465/08.
DR N-PSDB; ADI24485.
XX
PT Identifying a candidate Chk1 pathway modulating agent for treating e.g.,
PT cancer, comprises contacting an assay system comprising a MCHK
PT polypeptide or nucleic acid with a test agent and detecting a test agent-
PT biased activity.
XX
FS Example; SEQ ID NO 85; 266pp; English.
XX
CC The present invention describes a method for identifying a candidate Chk1
CC pathway modulating agent. The method comprises: (a) providing an assay
CC system comprising a modifier of Chk1 (MCHK) polypeptide or nucleic acid;
CC (b) contacting the system with a test agent, where the system provides a
CC reference activity except in the presence of the test agent; and (c)

CC detecting a test agent-biased activity, and a difference between the test
 CC agent-biased activity and the reference activity. Also described: (1) a
 CC method for modulating Chk1 pathway of a cell; (2) a method for modulating
 CC Chk1 pathway in a mammalian cell; and (3) a method for diagnosing a
 CC disease in a patient. A MCHK sequence has cytostatic activity, and can be
 CC used in gene therapy. The method is useful for identifying a candidate
 CC Chk1 pathway-modulating agent for preparing a composition for diagnosing
 CC or treating e.g., cancer. The present sequence represents a human MCHK
 CC protein, which is used in the exemplification of the present invention.
 XX
 SQ .Sequence 166 AA;

Query Match 100.0%; Score 846; DB 8; Length 166;
 Best Local Similarity 100.0%; Pred. No. 1.4e-83;
 Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MASGVAVSDGVIVKVFNDMKVRKSTPEEVKKRKAFLFCLSEDKNIIIEEGKEIILVGDV 60
 DB 1 MASGVAVSDGVIVKVFNDMKVRKSTPEEVKKRKAFLFCLSEDKNIIIEEGKEIILVGDV 60
 QY 61 GOTVDDPYATFVKMLPDKCRVALYDATYETKESKEDLVFIFWAPESAPLKSMMIYASS 120
 DB 61 GOTVDDPYATFVKMLPDKCRVALYDATYETKESKEDLVFIFWAPESAPLKSMMIYASS 120
 QY 121 KDAIKKLTGIRKHELQANCYEEVKDRCTLAELKGGSAVISLEGKPL 166
 DB 121 KDAIKKLTGIRKHELQANCYEEVKDRCTLAELKGGSAVISLEGKPL 166

RESULT 4
 ADO05889
 ID ADO05889 standard; protein; 166 AA.
 AC ADO05889;
 DT 15-JUL-2004 (first entry)
 XX Human cofilin polypeptide.
 DE Cofilin; inflammatory disease; antiasthmatic; human.
 KW Cofilin; inflammatory disease; antiasthmatic; human.
 XX Homo sapiens.
 OS Homo sapiens.
 PN WO2004035092-A2.
 XX 29-APR-2004.
 XX 15-OCT-2003; 2003WO-GB004450.
 XX 15-OCT-2002; 2002GB-00024014.
 XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 PA (FARB) BAYER HEALTHCARE AG.
 XX Bacon KB, Herath HMA, Liu N, Rohlf C;
 PI WPI; 2004-348336/32.
 DR N-PSDB; ADO05890.
 XX Treating or preventing an inflammatory disease, e.g., asthma comprises
 PT administering to a subject an agonist or antagonist of cofilin isoform 1
 PT or 2 that modulates the expression or activity of a cofilin polypeptide.
 XX Claim 6; SEQ ID NO 1; 47pp; English.
 PS The invention relates to treating or preventing an inflammatory disease
 CC and involves administering to a subject, an agent that modulates the
 CC expression or activity of a cofilin polypeptide. The agent is an agonist
 CC or antagonist of cofilin isoform 1 or 2. Antiasthmatic. The method is
 CC useful in treating or preventing an inflammatory disease, e.g., asthma.
 CC The present sequence represents a human cofilin polypeptide.
 XX Sequence 166 AA;
 XX

Query Match 100.0%; Score 846; DB 8; Length 166;
 Best Local Similarity 100.0%; Pred. No. 1.4e-83;
 Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MASGVAVSDGVIVKVFNDMKVRKSTPEEVKKRKAFLFCLSEDKNIIIEEGKEIILVGDV 60
 DB 1 MASGVAVSDGVIVKVFNDMKVRKSTPEEVKKRKAFLFCLSEDKNIIIEEGKEIILVGDV 60
 QY 61 GOTVDDPYATFVKMLPDKCRVALYDATYETKESKEDLVFIFWAPESAPLKSMMIYASS 120
 DB 61 GOTVDDPYATFVKMLPDKCRVALYDATYETKESKEDLVFIFWAPESAPLKSMMIYASS 120
 QY 121 KDAIKKLTGIRKHELQANCYEEVKDRCTLAELKGGSAVISLEGKPL 166
 DB 121 KDAIKKLTGIRKHELQANCYEEVKDRCTLAELKGGSAVISLEGKPL 166

RESULT 5
 ADO30534
 ID ADO30534 standard; protein; 166 AA.
 XX ADO30534;
 AC ADO30534;
 DT 23-SEP-2004 (first entry)
 XX Pancreas cancer marker - non-muscle cofilin isoform.
 DE Cytostatic; diagnosis; pancreatic cancer; antibody; antisense construct;
 KW differential expression.
 XX Homo sapiens.
 OS Homo sapiens.
 PN WO2004055519-A2.
 XX 01-JUL-2004.
 PD 11-DEC-2003; 2003WO-EP014057.
 PF 17-DEC-2002; 2002EP-00028058.
 PR 05-NOV-2003; 2003EP-00025237.
 XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
 PA (SINO-) SINOGENOMAX CO LTD CHINESE NAT HUMAN GEN.
 XX Chen J, Hu L, Liu TH, Lu ZH, Shen Y;
 PI WPI; 2004-488121/46.
 DR New specific markers comprises at least one polypeptide up-regulated in
 PT pancreatic cancer, useful for diagnosing pancreatic cancer.
 XX Claim 1; SEQ ID NO 21; 381pp; English.
 XX The invention relates to a marker (I) for diagnosis of pancreatic cancer
 CC comprising at least one polypeptide selected from 55 proteins up-
 CC regulated in pancreatic cancer (Table 2 and Table 3, given in the
 CC specification) or from 68 proteins with higher levels in pancreatic
 CC cancer compared to normal tissue (Table 6, given in the specification).
 CC (I) is a polypeptide for use as a marker or as a component of a marker
 CC for diagnosis of pancreatic cancer and/or the susceptibility to
 CC pancreatic cancer. A compound (antibody, an antibody-derivative, an
 CC antibody fragment, a peptide, or an antisense construct) identified by
 CC screening methods using (I) is useful for treatment or prevention of
 CC pancreatic cancer. It is also useful for the preparation of a diagnostic
 CC composition for diagnosing pancreatic cancer or a predisposition for
 CC pancreatic cancer. The current polypeptides were found to be
 CC differentially expressed in pancreatic tissue obtained from individuals
 CC suffering from pancreatic cancer as compared to healthy pancreatic
 CC tissue. They have been identified as suitable as markers of pancreatic
 CC cancer for early diagnosis of the disease. This sequence corresponds to a
 CC protein marker of the invention.
 XX

SQ Sequence 166 AA;		Query Match 100.0%; Score 846; DB 8; Length 166;	
		Best Local Similarity 100.0%; Pred. No. 1.4e-83;	
		Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 MASGVAVSDGVIKVFNDMKVRKSTPEEVKKRKAVALFCLSEDKNNILLEGKILVGDV 60		
Db	1 MASGVAVSDGVIKVFNDMKVRKSTPEEVKKRKAVALFCLSEDKNNILLEGKILVGDV 123		
Qy	61 GQTVDDPYATFVKMLPKDCRYALYDATYETKESKEDLVFIWAPESAPLKSMIYASS 120		
Db	61 GQTVDDPYATFVKMLPKDCRYALYDATYETKESKEDLVFIWAPESAPLKSMIYASS 183		
Qy	121 KDAIKKLTGKIKHELOANCYEEVKDRCTLAELGSGSAVISLEGKPL 166		
Db	121 KDAIKKLTGKIKHELOANCYEEVKDRCTLAELGSGSAVISLEGKPL 229		
RESULT 6		RESULT 7	
ID	ADQ65133 standard; protein; 229 AA.	ID	ABR41637 standard; protein; 187 AA.
XX	AC ADQ65133;	XX	AC ABR41637;
DT	07-OCT-2004 (first entry)	DT	02-JUN-2003 (first entry)
DE	Novel human protein sequence #106.	DE	Human DITHP cytoskeletal protein.
KW	osteopathic; neuroprotective; neurotropic; antiparkinsonian; cytostatic;	KW	Human; dithp; diagnostic and therapeutic polynucleotide; diagnosis;
KW	gene therapy; diagnostic marker; morbid state; osteoporosis;	KW	cancer; cell proliferative disorder; autoimmune disorder;
KW	neurological disease; Alzheimer's disease; Parkinson's disease; dementia;	KW	inflammatory disorder; infection; hormonal disorder; metabolic disorder;
KW	cancer.	KW	neurological disorder; gastrointestinal disorder; transport disorder;
OS	Homo sapiens.	KW	connective tissue disorder; drug screening; proteomic analysis;
XX	EP1440981-A2.	KW	gene therapy; antisense therapy; genotyping; transgenic animal; knock in;
XX	28-JUL-2004.	KW	disease model; toxicological testing; transcript imaging;
XX	21-JAN-2004; 2004EP-00001196.	XX	cytoskeletal protein.
XX	21-JAN-2003; 2003JP-00102206.	OS	Homo sapiens.
PR	09-MAY-2003; 2003JP-00131392.	XX	WO200297031-A2.
XX	(REAS-) RES ASSOC BIOTECHNOLOGY.	PN	05-DEC-2002.
FA	Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;	PF	27-MAR-2002; 2002WO-US010056.
PI	Yamamoto J, Isono Y, Nagai K, Irie R;	PR	28-MAR-2001; 2001US-0279619P.
XX	WPI; 2004-533376/52.	PR	29-MAR-2001; 2001US-0280067P.
DR	N-PSDB; ADQ62945.	PR	29-MAR-2001; 2001US-0280068P.
XX	Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases,	PR	16-MAY-2001; 2001US-0291280P.
PT	Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.	PR	17-MAY-2001; 2001US-0291829P.
PS	Claim 1; SEQ ID NO 2294; 2449pp; English.	PR	19-JUN-2001; 2001US-0299428P.
XX	The invention relates to 2495 novel polynucleotides (I) and their encoded	PR	20-JUN-2001; 2001US-0299776P.
CC	polypeptides, sequences hybridizing to these nucleotides, sequences	XX	(INCY-) INCYTE GENOMICS INC.
CC	encoding partial polypeptides and sequences having 70% or 90% identity to	XX	Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
CC	the nucleotide and protein sequences. The nucleotides and polypeptides	PI	Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Ameshey SR;
CC	are useful as diagnostic markers or therapeutic target for the diseases	PI	Daughterly SC, Dam TC, Liu TF, Nguyen DA, Klesfeld Y, Gerstin EH;
CC	or morbid states. They are also useful for treating osteoporosis,	PI	Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
CC	neurological diseases, Alzheimer's diseases, Parkinson's diseases,	PI	Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;
CC	dementia and various cancers. This sequence corresponds to a protein	XX	WPI; 2003-129518/12.
CC	sequence of the invention.	DR	N-PSDB; ACC46574.
XX	Sequence 229 AA;	XX	Novel human diagnostic and therapeutic polypeptide useful for identifying
Qy	Query Match 100.0%; Score 846; DB 8; Length 229;	PT	test compound which specifically binds to a polypeptide encoded by human
Best Local Similarity 100.0%; Pred. No. 2.2e-83;		PT	diagnostic and therapeutic polynucleotide, and to induce antibodies.
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		PS	Claim 27; SEQ ID NO 1172; 591pp; English.
		XX	The invention relates to novel human diagnostic and therapeutic
		CC	polynucleotides designated dithp (ACC46080-ACC46749) and to their encoded
		CC	proteins (DITHP; ABR41136-ABR41812). The invention also relates to
		CC	polynucleotide sequences at least 90% identical to the dithp cDNA
		CC	sequences of the invention; recombinant vectors, host cells and

Sequence 187 AA;

PR	17-JAN-2003	2003US-04408200P	PR
PR	17-JAN-2003	2003US-04408201P	PR
PR	17-JAN-2003	2003US-04408202P	PR
PR	18-APR-2003	2003US-0463700P	PR
PR	18-APR-2003	2003US-04637008P	PR
PR	18-APR-2003	2003US-0463708P	PR
PR	18-APR-2003	2003US-0463716P	PR
PR	18-APR-2003	2003US-04637162P	PR
PR	18-APR-2003	2003US-0463732P	PR
PR	02-MAY-2003	2003US-0467199P	PR
PR	02-MAY-2003	2003US-0467201P	PR
PR	02-MAY-2003	2003US-0467203P	PR
PR	02-MAY-2003	2003US-0467230P	PR
PR	19-MAY-2003	2003US-0471306P	PR
PR	19-MAY-2003	2003US-0471336P	PR
PR	19-MAY-2003	2003US-04713362P	PR
PR	22-MAY-2003	2003US-0472420P	PR
PR	22-MAY-2003	2003US-0472430P	PR
PR	09-JUN-2003	2003US-0476609P	PR
PR	09-JUN-2003	2003US-0476621P	PR
PR	09-JUN-2003	2003US-0476632P	PR
PR	09-JUN-2003	2003US-0476641P	PR
PR	08-JUL-2003	2003US-0485217P	PR
PR	08-JUL-2003	2003US-0485218P	PR
PR	08-JUL-2003	2003US-0485223P	PR
PR	08-JUL-2003	2003US-0485224P	PR
PR	08-JUL-2003	2003US-0485325P	PR
PR	08-JUL-2003	2003US-0485359P	PR
PR	14-JUL-2003	2003US-0486446P	PR
PR	14-JUL-2003	2003US-0486480P	PR
PR	14-JUL-2003	2003US-0486849P	PR
PR	15-JUL-2003	2003US-0486891P	PR
PR	15-JUL-2003	2003US-0486960P	PR
PR	08-AUG-2003	2003US-0493341P	PR
PR	08-AUG-2003	2003US-0493370P	PR
PR	08-AUG-2003	2003US-0493573P	PR
PR	08-AUG-2003	2003US-0493577P	PR

PK 03-JUN-2003, 2003US-0460411P,
PR 03-JUN-2003, 2003US-0485217P,
PR 03-JUN-2003, 2003US-0485218P,
PR 08-JUL-2003, 2003US-0485218P,
PR 08-JUL-2003, 2003US-0485223P,
PR 08-JUL-2003, 2003US-0485224P,
PR 08-JUL-2003, 2003US-0485325P,
PR 08-JUL-2003, 2003US-0485359P,
PR 14-JUL-2003, 2003US-0486446P,
PR 14-JUL-2003, 2003US-0486480P,
PR 15-JUL-2003, 2003US-0486891P,
PR 15-JUL-2003, 2003US-0489609P,
PR 08-AUG-2003, 2003US-0493341P,
PR 08-AUG-2003, 2003US-0493370P,
PR 08-AUG-2003, 2003US-0493573P,
PR 08-AUG-2003, 2003US-0493577P,

PR 08-JUL-2003; 2003US-04853359P
PR 14-JUL-2003; 2003US-0486446P
PR 14-JUL-2003; 2003US-0486480P
PR 15-JUL-2003; 2003US-0486819P
PR 15-JUL-2003; 2003US-0486960P
PR 08-AUG-2003; 2003US-0493341P
PR 08-AUG-2003; 2003US-0493370P
PR 08-AUG-2003; 2003US-0493557P
PR 08-AUG-2003; 2003US-0493577P

PR 15-JUL-2003; 2003US-0486891P.
PR 15-JUL-2003; 2003US-0486961P.
PR 14-JUL-2003; 2003US-0486480P.
PR 15-JUL-2003; 2003US-0486891P.
PR 15-JUL-2003; 2003US-0486961P.
PR 08-AUG-2003; 2003US-0493341P.
PR 08-AUG-2003; 2003US-0493370P.
PR 08-AUG-2003; 2003US-0493373P.
PR 08-AUG-2003; 2003US-0493577P.

PR 15-JUL-2003; 2003US-0486960P
PR 08-AUG-2003; 2003US-0493341P
PR 08-AUG-2003; 2003US-0493370P
PR 08-AUG-2003; 2003US-0493370P
PR 08-AUG-2003; 2003US-0493573P
PR 08-AUG-2003; 2003US-0493577P

(FIVE-) FIVE PRIME THERAPEUTICS INC.

Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;
PI Halenbeck RF, Kothakota S, Lin H, Linnemann T, Pierce K, Wang Y;
PI Wong JGP, Wu G, Zhang H, Zeng C;

PI Williams LT, Chu K, Lee E,
PI Halenbeck RF, Kothakota S,
PI Wong JGP, Wu G, Zhang H, Z

FI Wong JGF, Wu G, Zhang H, XX
DR WPI; 2004-365511/34.
DR N-PSDB: ADN99006.

WPI; 2004-365511/34.
N-PSDB: ADN99006.

XX New nucleic acid molecules. in

PT
treating or preventing e.g. i

PT disorders, cancer, psoriasis,

PT ulcerative colitis.

XX

PS Claim 14; SEQ ID NO 1390; 532pp; English.

XX CC The invention relates to a nucleic acid molecule comprising a

CC polynucleotide sequence or its complement that encodes a polypeptide. The

CC nucleic acid is useful in preparing a composition for treating or

CC preventing inflammatory, CNS, immune, bacterial or viral disorder,

CC cancer, psoriasis, diabetes, early aging, hormonal imbalance, ischemic

CC heart disease or ulcerative colitis. This sequence corresponds to a

CC protein of the invention.

XX SQ Sequence 239 AA;

Query Match 99.4%; Score 841; DB 8; Length 239;

Best Local Similarity 100.0%; Pred. No. 8.2e-83;

Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ASGVASDGVIVKFNDMKVRKSTPEEVKRRKAVLFCLSSEDKKNIILEGKEILVGDVG 61

Db 75 ASGVASDGVIVKFNDMKVRKSTPEEVKRRKAVLFCLSSEDKKNIILEGKEILVGDVG 134

Qy 62 QTVDPPYATFVKMLPDKDCRYALDYATYETKESKEDLVFIWAPESAPLKSKMIYASSK 121

Db 135 QTVDPPYATFVKMLPDKDCRYALDYATYETKESKEDLVFIWAPESAPLKSKMIYASSK 194

Qy 122 DAIKKLTGIGHELOANCYEEVKDRCTLAELKGGSAVISLEGKPL 166

Db 195 DAIKKLTGIGHELOANCYEEVKDRCTLAELKGGSAVISLEGKPL 239

RESULT 9

ID ADJ70464

ADJ70464 standard; protein; 149 AA.

XX AC ADJ70464;

XX DT 06-MAY-2004 (first entry)

XX DE Human heat mitochondrial protein as a therapeutic target SeqID2270.

XX KW mitochondrial; human; screening assay; diabetes mellitus;

XX KW Huntington's disease; osteoarthritis;

XX KW Leber's hereditary optic neuropathy; LHON;

XX KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;

XX KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;

XX KW neuroprotective; nontropic; antidiabetic; anticonvulsant; antiarthritic;

XX KW osteopathic; ophthalmological; cytostatic.

XX OS Homo sapiens.

XX PN WO2003087768-A2.

XX PD 23-OCT-2003.

XX PF 04-APR-2003; 2003WO-US010870.

XX PR 12-APR-2002; 2002US-0372843P.

XX PR 17-JUN-2002; 2002US-0389987P.

XX PR 20-SEP-2002; 2002US-0412418P.

XX PA (MITO-) MITOKOR.

XX PA (BUCK-) BUCK INST AGE RES.

XX PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;

PI Warnock DE;

XX DR WPI; 2003-845369/78.

XX PT Identifying a mitochondrial target for drug screening assays and for

PT treating diseases associated with altered mitochondrial function,

PT comprises detecting a modified polypeptide in a sample and correlating

PT with the disease.

XX PS Claim 1; SEQ ID NO 2270; 180pp; English.

XX CC This invention relates to novel mitochondrial targets that can be used

CC for therapeutic intervention in treating a disease associated with

CC altered mitochondrial function. Specifically, it refers to a method for

CC identifying proteins of the human heart mitochondrial proteome that are

CC useful for drug screening assays, as well as therapeutic targets. The

CC present invention describes a method for identifying such proteins that

CC can be used in the treatment of various diseases associated with altered

CC mitochondrial function including diabetes mellitus, Huntington's disease,

CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial

CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy

CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these

CC compositions have neuroprotective, nontropic, antidiabetic,

CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and

CC cytostatic activities. This polypeptide sequence is a human heart

CC mitochondrial protein of the invention.

XX SQ Sequence 149 AA;

Query Match 90.3%; Score 764; DB 7; Length 149;

Best Local Similarity 100.0%; Pred. No. 1e-74;

Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 MKVRKSTPEEVKRRKAVLFCLSSEDKKNIILEGKEILVGDVGQTVDDPYATFVKMLPD 77

Db 1 MKVRKSTPEEVKRRKAVLFCLSSEDKKNIILEGKEILVGDVGQTVDDPYATFVKMLPD 60

Qy 78 KDCRYALDYATYETKESKEDLVFIWAPESAPLKSKMIYASSKDAIKKLTGIGHELOA 137

Db 61 KDCRYALDYATYETKESKEDLVFIWAPESAPLKSKMIYASSKDAIKKLTGIGHELOA 120

Qy 138 NCYEEVKDRCTLAELKGGSAVISLEGKPL 166

Db 121 NCYEEVKDRCTLAELKGGSAVISLEGKPL 149

RESULT 10

ABR41956

ID ABR41956 standard; protein; 166 AA.

XX AC ABR41956;

XX DT 11-AUG-2003 (first entry)

XX DE Mouse cofillin, implicated in pain.

XX KW Mouse; cofillin; nociceptive; analgesic; signal transduction;

XX KW transgenic animal.

XX OS Mus musculus.

XX PN EP1281775-A2.

XX PD 05-FEB-2003.

XX PF 26-JUL-2002; 2002EP-00255231.

XX PR 27-JUL-2001; 2001GB-00018354.

XX PR 07-FEB-2002; 2002GB-00002892.

XX PA (WARN) WARNER LAMBERT CO.

XX PI Brooksbank RA, Dixon AK, Lee K, Pinnock RD;

XX DR WPI; 2003-335009/32.

XX DR N-PSDB; ACC48821.

XX PT Use of isolated gene or nucleic acid sequence, recombinant vector, host

PT cell, non-human animal, polypeptide encoded by the nucleic acid sequence,

PT or antibody, for screening of compounds for the treatment of pain, or for

PT diagnosing pain.

XX PS Disclosure; Page 65-66; 87pp; English.

XX The present sequence is the protein sequence of mouse cofilin. This is
CC encoded by a gene that has been identified as being up-regulated in 2
CC models of chronic pain, i.e. streptozocin-induced diabetes and chronic
CC constrictive injury to a nerve leading to the spine. The expression
CC products of such genes can be used to screen libraries for compounds and
CC peptide agonists and antagonists of gene product activity that may be
CC useful in the treatment or prevention of chronic pain, and in the
CC characterisation of diagnostic tools for the identification and
XX characterisation of pain
SQ Sequence 166 AA;

Query Match 83.0%; Score 702; DB 6; Length 166;
Best Local Similarity 81.3%; Pred. No. 6.6e-68;
Matches 135; Conservative 14; Mismatches 17; Indels 0; Gaps 0;

QY 1 MASGVAVSDGVIVKVFNDMKVRKSTPEEVKKRKAVALFCLSEDKNIIILEEGKEIIVGDV 60
DB 1 MASGVTVNDEVIKVFNDMKVRKSTQEEIKRKAVALFCLSDDDKQRIIVEEAKQIIVGDI 60
QY 61 GQTVDDPYATFVKMLPDKCRYALYDATYETKESKKEDLVFIWAPESAPLKSMMIYASS 120
DB 61 GQTVDDPYATFVKMLPDKCRYALYDATYETKESKKEDLVFIWAPESAPLKSMMIYASS 120
QY 121 KDAIKKKLTGIRKHELQANCYEEVKDRTLAELKGGSAVISLECKPL 166
DB 121 KDAIKKKLTGIRKHELQANCYEEVKDRTLAELKGGSAVISLECKPL 166

RESULT 11
AAW78545
ID AAW78545 standard; protein; 166 AA.
AC AAW78545;
XX
XX
XX 06-NOV-2001 (first entry)
DE Human protein SEQ ID NO 1207.
XX
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
XX vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
XX tissue growth factor; immunomodulatory; cancer; leukaemia;
XX nervous system disorder; arthritis; inflammation.
XX
XX Homo sapiens.
XX
XX WO200157190-A2.
XX
XX 09-AUG-2001.
XX
XX 05-FEB-2001; 2001WO-US004098.
XX
XX 03-FEB-2000; 2000US-00496914.
XX 27-APR-2000; 2000US-00560875.
XX 20-JUN-2000; 2000US-00598075.
XX 19-JUL-2000; 2000US-00620325.
XX 01-SEP-2000; 2000US-00654936.
XX 15-SEP-2000; 2000US-00663561.
XX 30-OCT-2000; 2000US-00693325.
XX 30-NOV-2000; 2000US-00728422.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
XX Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
XX Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
XX WPI: 2001-476283/51.
XX N-PSDB: AAK51678.
XX
XX Nucleic acids encoding polypeptides with cytokine-like activities, useful
XX in diagnosis and gene therapy.

XX Claim 20; Page 3461-3462; 6221pp; English.
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78123-AAM80302) that exhibit activity relating to
CC cytokines, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activity/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
CC sequence listing were missing at the time of publication
XX
SQ Sequence 166 AA;

Query Match 82.6%; Score 699; DB 4; Length 166;
Best Local Similarity 80.7%; Pred. No. 1.4e-67;
Matches 134; Conservative 15; Mismatches 17; Indels 0; Gaps 0;

QY 1 MASGVAVSDGVIVKVFNDMKVRKSTPEEVKKRKAVALFCLSEDKNIIILEEGKEIIVGDV 60
DB 1 MASGVTVNDEVIKVFNDMKVRKSTQEEIKRKAVALFCLSDDDKQRIIVEEAKQIIVGDI 60
QY 61 GQTVDDPYATFVKMLPDKCRYALYDATYETKESKKEDLVFIWAPESAPLKSMMIYASS 120
DB 61 GQTVDDPYATFVKMLPDKCRYALYDATYETKESKKEDLVFIWAPESAPLKSMMIYASS 120
QY 121 KDAIKKKLTGIRKHELQANCYEEVKDRTLAELKGGSAVISLECKPL 166
DB 121 KDAIKKKLTGIRKHELQANCYEEVKDRTLAELKGGSAVISLECKPL 166

RESULT 12
ADB75248
ID ADB75248 standard; protein; 166 AA.
XX
XX ADB75248;
XX
XX 04-DEC-2003 (first entry)
XX
XX Prostate cancer marker protein.
XX
XX Prostate; cancer; cytostatic; gene therapy; marker.
XX
XX Homo sapiens.
XX
XX WO2003009814-A2.
XX
XX 06-FEB-2003.
XX
XX 25-JUL-2002; 2002WO-US023913.
XX
XX 25-JUL-2001; 2001US-0307982P.
XX 22-AUG-2001; 2001US-0314356P.
XX 25-SEP-2001; 2001US-0325020P.
XX 12-DEC-2001; 2001US-0341746P.
XX 05-MAR-2002; 2002US-0362158P.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Schlegel R, Monahan JE, Endege WO, Gannavarapu M, Gorbacheva B;
XX Hoersht S, Kanatkar S, Wonsley AM, Glatt K, Zhao X, Anderson D;
XX
XX WPI: 2003-248033/24.
XX
XX New nucleic acid molecule, useful for diagnosing or treating prostate
XX cancer.
XX
XX Disclosure; SEQ ID NO 72; 99pp; English.

XX The invention relates to newly discovered cancer markers associated with
 CC the cancerous state of prostate cells. Also disclosed is a method of
 CC assessing whether a patient is afflicted with prostate cancer. The method
 CC of the invention involves assessing whether a patient is afflicted with
 CC prostate cancer by comparing the level of expression of a marker in a
 CC patient sample and the normal level of expression of the marker in a
 CC control non-prostate cancer sample, where a significant increase in the
 CC level of expression of the marker in the patient sample and the normal
 CC nucleic acids of the invention are useful for diagnosing or treating
 CC prostate cancer, and may be useful in gene therapy. Sequences given in
 CC ADB75177-ADB75631 represent marker cDNA and proteins. Note: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 166 AA;
 Query Match 82.6%; Score 699; DB 7; Length 166;
 Best Local Similarity 80.7%; Pred. No. 1.4e-67;
 Matches 134; Conservative 15; Mismatches 17; Indels 0; Gaps 0;
 QY 1 MASGVAVSDGVKVFNDKVRKSTPEEVKRRKAVLFCLSDDKQRIIVEEAKQILVGDV 60
 DB 1 MASGVTVNDEVKVFNDKVRKSTQEEIKRRKAVLFCLSDDKQRIIVEEAKQILVGDV 60
 QY 61 GQTVDDPYATFVKMLPDKCRYALDYATYETKESKEDLVFIWAPESAPLKSKMIYASS 120
 DB 61 GDTVEDPYTSFVKLLPLNDCRYALDYATYETKESKEDLVFIWAPESAPLKSKMIYASS 120
 QY 121 KDAIKKLTGKHLEQANCYEEVKDRCTLAELGGSVAISLEGKPL 166
 DB 121 KDAIKKFTGKHLEQANCYEEVKDRCTLAELGGSVAISLEGKPL 166
 RESULT 13
 ADJ70104
 ID ADJ70104 standard; protein; 166 AA.
 AC ADJ70104;
 XX
 XX 06-MAY-2004 (first entry)
 XX Human heat mitochondrial protein as a therapeutic target SeqID1910.
 XX mitochondrial; human; screening assay; diabetes mellitus;
 KW Huntington's disease; osteoarthritis;
 KW Leber's hereditary optic neuropathy; LHON;
 KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
 KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
 KW neuroprotective; neurotropic; antidiabetic; anticonvulsant; antiarthritic;
 KW osteopathic; ophthalmological; cytostatic.
 XX Homo sapiens.
 OS
 XX WO2003087768-A2.
 XX
 XX 23-OCT-2003.
 XX
 XX 04-APR-2003; 2003WO-US010870.
 XX
 XX 12-APR-2002; 2002US-0372843P.
 XX 17-JUN-2002; 2002US-039987P.
 XX 20-SEP-2002; 2002US-0412418P.
 XX
 XX (MITO-) MITOKOR.
 XX (BUCK-) BUCK INST AGE RES.
 XX
 XX Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
 XX Warnock DE;
 XX WPI; 2003-845369/78.

XX Identifying a mitochondrial target for drug screening assays and for
 PT treating diseases associated with altered mitochondrial function,
 PT comprises detecting a modified polypeptide in a sample and correlating
 PT with the disease.
 XX
 PS Claim 1; SEQ ID NO 1910; 180pp; English.
 XX
 CC This invention relates to novel mitochondrial targets that can be used
 CC for therapeutic intervention in treating a disease associated with
 CC altered mitochondrial function. Specifically, it refers to a method for
 CC identifying proteins of the human heart mitochondrial proteome that are
 CC useful for drug screening assays, as well as therapeutic targets. The
 CC present invention describes a method for identifying such proteins that
 CC can be used in the treatment of various diseases associated with altered
 CC mitochondrial function including diabetes mellitus, Huntington's disease,
 CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
 CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
 CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
 CC compositions have neuroprotective, neurotropic, antidiabetic,
 CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
 CC cytostatic activities. This polypeptide sequence is a human heart
 CC mitochondrial protein of the invention.
 XX
 SQ Sequence 166 AA;
 Query Match 82.6%; Score 699; DB 7; Length 166;
 Best Local Similarity 80.7%; Pred. No. 1.4e-67;
 Matches 134; Conservative 15; Mismatches 17; Indels 0; Gaps 0;
 QY 1 MASGVAVSDGVKVFNDKVRKSTPEEVKRRKAVLFCLSDDKQRIIVEEAKQILVGDV 60
 DB 1 MASGVTVNDEVKVFNDKVRKSTQEEIKRRKAVLFCLSDDKQRIIVEEAKQILVGDV 60
 QY 61 GQTVDDPYATFVKMLPDKCRYALDYATYETKESKEDLVFIWAPESAPLKSKMIYASS 120
 DB 61 GDTVEDPYTSFVKLLPLNDCRYALDYATYETKESKEDLVFIWAPESAPLKSKMIYASS 120
 QY 121 KDAIKKLTGKHLEQANCYEEVKDRCTLAELGGSVAISLEGKPL 166
 DB 121 KDAIKKFTGKHLEQANCYEEVKDRCTLAELGGSVAISLEGKPL 166
 RESULT 14
 ADI24536
 ID ADI24536 standard; protein; 166 AA.
 XX
 AC ADI24536;
 XX
 DT 15-APR-2004 (first entry)
 XX Human modifier of Chk1 (MCHK) protein SEQ ID NO:86.
 DE Chk1 pathway modulating agent; modifier of Chk1; MCHK; cytostatic;
 XX gene therapy; cancer; human.
 KW
 KW Homo sapiens.
 OS
 XX WO2004004785-A1.
 XX
 XX 15-JAN-2004.
 XX
 XX 09-JUL-2003; 2003WO-US021379.
 XX
 XX 10-JUL-2002; 2002US-0394845P.
 XX 16-SEP-2002; 2002US-0410986P.
 XX
 XX (EXEL-) EXELIXIS INC.
 XX
 XX Francis-Lang H, Roche S, Joo DM, Nicoll M, Hai B, Zhang H;
 PI Lickteig K, Amundsen CD, Jin Y, Adamkewicz JI, Platt DM;
 PI Hammonds RG;
 XX

PR 02-OCT-2000; 2000US-0236802P.
 PR 02-OCT-2000; 2000US-0237037P.
 PR 02-OCT-2000; 2000US-0237038P.
 PR 02-OCT-2000; 2000US-0237039P.
 PR 02-OCT-2000; 2000US-0237040P.
 PR 13-OCT-2000; 2000US-0239935P.
 PR 13-OCT-2000; 2000US-0239937P.
 PR 20-OCT-2000; 2000US-0240960P.
 PR 20-OCT-2000; 2000US-0241221P.
 PR 20-OCT-2000; 2000US-0241785P.
 PR 20-OCT-2000; 2000US-0241786P.
 PR 20-OCT-2000; 2000US-0241787P.
 PR 20-OCT-2000; 2000US-0241808P.
 PR 20-OCT-2000; 2000US-0241809P.
 PR 20-OCT-2000; 2000US-0241836P.
 PR 01-NOV-2000; 2000US-0244617P.
 PR 08-NOV-2000; 2000US-0246474P.
 PR 08-NOV-2000; 2000US-0246475P.
 PR 08-NOV-2000; 2000US-0246476P.
 PR 08-NOV-2000; 2000US-0246477P.
 PR 08-NOV-2000; 2000US-0246524P.
 PR 08-NOV-2000; 2000US-0246525P.
 PR 08-NOV-2000; 2000US-0246526P.
 PR 08-NOV-2000; 2000US-0246527P.
 PR 08-NOV-2000; 2000US-0246528P.
 PR 08-NOV-2000; 2000US-0246532P.
 PR 08-NOV-2000; 2000US-0246609P.
 PR 08-NOV-2000; 2000US-0246610P.
 PR 08-NOV-2000; 2000US-0246611P.
 PR 08-NOV-2000; 2000US-0246613P.
 PR 17-NOV-2000; 2000US-0249207P.
 PR 17-NOV-2000; 2000US-0249208P.
 PR 17-NOV-2000; 2000US-0249209P.
 PR 17-NOV-2000; 2000US-0249210P.
 PR 17-NOV-2000; 2000US-0249211P.
 PR 17-NOV-2000; 2000US-0249212P.
 PR 17-NOV-2000; 2000US-0249213P.
 PR 17-NOV-2000; 2000US-0249214P.
 PR 17-NOV-2000; 2000US-0249215P.
 PR 17-NOV-2000; 2000US-0249216P.
 PR 17-NOV-2000; 2000US-0249217P.
 PR 17-NOV-2000; 2000US-0249218P.
 PR 17-NOV-2000; 2000US-0249244P.
 PR 17-NOV-2000; 2000US-0249245P.
 PR 17-NOV-2000; 2000US-0249254P.
 PR 17-NOV-2000; 2000US-0249256P.
 PR 17-NOV-2000; 2000US-0249257P.
 PR 17-NOV-2000; 2000US-0249297P.
 PR 17-NOV-2000; 2000US-0249299P.
 PR 01-DEC-2000; 2000US-0250160P.
 PR 01-DEC-2000; 2000US-0250391P.
 PR 05-DEC-2000; 2000US-0251030P.
 PR 05-DEC-2000; 2000US-0251988P.
 PR 05-DEC-2000; 2000US-0256719P.
 PR 06-DEC-2000; 2000US-0251479P.
 PR 08-DEC-2000; 2000US-0251856P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251869P.
 PR 08-DEC-2000; 2000US-0251989P.
 PR 08-DEC-2000; 2000US-0251990P.
 PR 11-DEC-2000; 2000US-0254097P.
 PR 05-JAN-2001; 2001US-0259678P.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-476182/51.

N-PSDB; AAS29808.

Novel isolated human cytoskeletal element-related polypeptide useful for

PT diagnosis/treatment of neoplastic disorders, disorders associated with
 XX neural transmission, chromosomal abnormalities, autoimmune disorders.
 PS Claim 11; SEQ ID NO 93; 505pp; English.
 XX
 CC Sequences AAU18508-AAU18551 represent the cytoskeletal element-related
 CC polypeptides of the invention. Cytoskeletal polypeptides and their
 CC associated polynucleotides are useful in the diagnosis, treatment and
 CC prevention of various types of disorders in e.g. humans, mice, rabbits,
 CC goats, horses, cats, dogs, chickens or sheep. A pathological condition
 CC can be determined by determining the presence or absence of a mutation in
 CC a cytoskeletal polynucleotide. The treatable disorders include autoimmune
 CC diseases such as rheumatoid arthritis, hyperproliferative disorders such
 CC as neoplasms of the breast or liver, cardiovascular disorders such as
 CC cardiac arrest, cerebrovascular disorders such as cerebral ischaemia,
 CC nervous system disorders such as Alzheimer's disease, infections caused
 CC by bacteria, viruses and fungi, ocular disorders such as corneal
 CC infection, endocrine disorders such as premature labour and infertility,
 CC gastrointestinal disorders such as Crohn's disease, renal disorders such
 CC as glomerulonephritis and respiratory disorders such as asthma. The
 CC polypeptides can also be used to aid wound healing, to prevent skin aging
 CC due to sunburn, to maintain organs before transplantation, to regenerate
 CC tissues and in chemotaxis. The polypeptides can also be used as a food
 CC additive or preservative to increase or decrease storage capabilities.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences

Query Match 82.6%; Score 699; DB 4; Length 205;
 Best Local Similarity 80.7%; Pred. No. 1.9e-67;
 Matches 134; Conservative 15; Mismatches 17; Indels 0; Gaps 0;
 QY 1 MASGVAVSDGVKVFNDMKVKRSTPEEVKKKAVLFCLSDKKNIIIEGKEILYGDV 60
 Db 40 MASGVTVNDEVIKVFNDMKVKRSTQEEIKKKKAVLFCLSDKQRIIVVEAKQILVGD 99
 QY 61 GQTVDDPYATFVKMLPDKCRYALYDITYETKESKKEDLVFIWAPESAPLKSMIYASS 120
 Db 100 GDTVEDPYTGFVKLLPLNDCRYALYDITYETKESKKEDLVFIWAPESAPLKSMIYASS 159
 QY 121 KDAIKKKLTGIIKHELQANCYEEVKDRCTLAELKGGSAVISLEGKPL 166
 Db 160 KDAIKKKFTGIRHEWQVNGLLDKRSTLGEKLGNNVVSLEGKPL 205

Search completed: May 13, 2005, 09:43:49
 Job time : 164 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 13, 2005, 09:37:55 ; Search time 38 Seconds
(without alignments)
420.315 Million cell updates/sec

Title: US-10-649-952A-1
Perfect score: 846
Sequence: 1 MASGVAVSDGVKVFNDMKV.....CTLAEKLGGSAVISLEGRPL 166
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	846	100.0	166	1 S12632	cofilin - human
2	842	99.5	166	2 S49101	cofilin - rat
3	841	99.4	166	1 A29240	cofilin - pig
4	839	99.2	166	1 S12584	cofilin - mouse
5	702	83.0	166	2 A53812	cofilin, muscle -
6	701	82.9	166	1 B35703	cofilin - chicken
7	620.5	73.3	165	1 A35702	destrin - chicken
8	606.5	71.7	165	1 A35179	destrin - pig
9	606.5	71.7	165	1 A54184	destrin [validated
10	598.5	70.7	164	2 JE0223	destrin - rat
11	267.5	31.6	143	1 A43397	cofilin - yeast (S
12	254	30.0	137	2 T43245	probable actin-dep
13	227	26.8	139	2 T02914	actin-depolymmerizi
14	213	25.2	140	2 A86149	actin-depolymmerizi
15	208	24.6	132	2 G84717	actin-depolymmerizi
16	208	24.6	139	2 T02883	actin-depolymmerizi
17	205.5	24.3	142	2 S71361	actin-binding prot
18	201.5	23.8	148	2 A57569	actin-depolymmerizi
19	200.5	23.7	133	2 T01232	actin-depolymmerizi
20	200.5	23.7	139	2 S03935	actin-depolymmerizi
21	195.5	23.1	130	2 T47540	actin-depolymmerizi
22	195	23.0	130	2 T05767	actin-depolymmerizi
23	192.5	22.8	139	2 T02882	actin-depolymmerizi
24	191	22.6	126	2 S03934	actin-depolymmerizi
25	190.5	22.5	130	2 T05788	actin-depolymmerizi
26	187	22.1	132	2 B84543	actin-depolymmerizi
27	185.5	21.9	135	2 T49327	cofilin related pr
28	176.5	20.9	58	2 A56448	destrin-like prote
29	158.5	18.7	133	2 T47539	actin-depolymmerizi

30	157.5	18.6	49	2 B56448	cofilin-like prote
31	150.5	17.8	165	2 S41728	actin depolymmerizi
32	149.5	17.7	293	2 T33952	actin depolymmerizi
33	130	15.4	152	2 S41727	unc-60 protein - C
34	120	14.2	350	2 A55922	tyrosine kinase A6
35	104	12.3	349	2 T46362	probable tyrosine
36	98.5	11.6	358	2 T13017	hypothetical prote
37	98	11.6	328	2 T40910	probable tyrosine
38	96.5	11.4	142	1 PT0410	glia maturation fa
39	96	11.3	141	1 JDB08	glia maturation fa
40	94	11.1	141	1 S22149	glia maturation fa
41	94	11.1	390	2 H64603	probable aspartate
42	86.5	10.2	350	2 T05589	hypothetical prote
43	86.5	10.2	418	2 E64100	probable ATP-depen
44	85.5	10.1	415	2 T34156	hypothetical prote
45	85.5	10.1	509	2 T29291	hypothetical prote

ALIGNMENTS

RESULT 1

S12632
cofilin - human
C:Species: Homo sapiens (man)
C:Date: 03-Feb-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C:Accession: S12632
R:Ogawa, K.; Tashima, M.; Yumoto, Y.; Okuda, T.; Sawada, H.; Okuma, M.; Maruyama, Y.
Nucleic Acids Res. 18, 7169, 1990
A:Title: Coding sequence of human placenta Cofilin cDNA.
A:Reference number: S12632; MUID:91088330; PMID:2263493
A:Accession: S12632
A:Molecule type: mRNA
A:Residues: 1-166 <OGA>
A:Cross-references: UNIPROT:P23528; EMBL:D00682; NID:g219544; RIDN:BA00589.1; PID:g21954
C:Comment: Cofilin reversibly regulates actin polymerization and depolymerization in a pr
C:Genetics:
A:Gene: GDB:CFL1; CFL
A:Cross-references: GDB:126798; OMIM:601442
A:Map position: 11q13-11q13
C:Superfamily: cofilin
C:Keywords: actin binding; phosphoprotein
F:26-36/Region: nuclear location signal
F:104-134/Region: actin binding #status predicted

Query Match	100.0%	Score	846;	DB	1;	Length	166;
Best Local Similarity	100.0%	Pred. No.	4.8e-61;	Mismatches	0;	Indels	0;
Matches	166;	Conservative	0;				
QY	1	MASGVAVSDGVKVFNDMKVKRSSTPEEVKRRKKA	VLFCLSEDKKNIILEEGKEILVGDV	60			
DB	1	MASGVAVSDGVKVFNDMKVKRSSTPEEVKRRKKA	VLFCLSEDKKNIILEEGKEILVGDV	60			
QY	61	GQTVDPPATFYKMLPDKDCRYALYDATYETKESK	KEDLVFIWAPESAPLKSMMIYAS	120			
DB	61	GQTVDPPATFYKMLPDKDCRYALYDATYETKESK	KEDLVFIWAPESAPLKSMMIYAS	120			
QY	121	KDAIKKLTGKHKEIQANCYEVRKDRCTLAELGGSA	VISLEGGKPL	166			
DB	121	KDAIKKLTGKHKEIQANCYEVRKDRCTLAELGGSA	VISLEGGKPL	166			

RESULT 2

S49101
cofilin - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Jan-1995 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
C:Accession: S49101; A58860; JE0222
R:Shirasawa, T.; Takahashi, H.; Sakamoto, K.; Kawashima, A.; Akashi, T.
submitted to the EMBL Data Library, October 1991
A:Description: Nucleotide sequence of rat cofilin cDNA.
A:Reference number: S49101
A:Accession: S49101

A:Molecule type: mRNA
A:Residues: 1-166 <SH1>
A:Cross-references: UNIPROT:P45592; EMBL:X62908; NID:G509200; PIDN:CAA44694.1; PID:G509202
R:Shirabawa, T.
Submitted to DBJ, October 1991
A:Reference number: A58860
A:Accession: A58860
A:Molecule type: mRNA
A:Residues: 1-166 <SH2>
A:Cross-references: EMBL:X62908; NID:G509200; PIDN:CAA44694.1; PID:G509201
A:Experimental source: embryo brain
R:Kanamori, T.; Suzuki, M.M.; Titani, K.
Submitted to JIPID, August 1998
A:Description: Complete amino acid sequences and phosphorylation sites, determined by Ed
A:Reference number: JE0222
A:Accession: JE0222
A:Molecule type: protein
A:Residues: 2-166 <KAN>
C:Superfamily: cofilin
C:Keywords: acetylated amino end; phosphoprotein
F:2-166/Product: cofilin #status experimental <MAT>
F:19-34/Region: nuclear location signal
F:104-115/Region: actin binding #status predicted
F:2/Modified site: acetylated amino end (Ala) (in mature form) #status experimental
F:3/Binding site: phosphate (Ser) (covalent) #status experimental

Query Match 99.5%; Score 842; DB 2; Length 166;
Best Local Similarity 99.4%; Pred. No. 1e-60;
Matches 165; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MASGVAVSDGVKVFNDMKVRSSTPEEVKKRKAVALFCLSEDKNNIILEGKEILVGDV 60
Db 1 MASGVAVSDGVKVFNDMKVRSSTPEEVKKRKAVALFCLSEDKNNIILEGKEILVGDV 60

Qy 61 GQTVDDPYATFVKMLPKDCRYALYDITYETKESKEDLVFIWAPESAPLKSKMIYASS 120
Db 61 GQTVDDPYTFVKMLPKDCRYALYDITYETKESKEDLVFIWAPESAPLKSKMIYASS 120

Qy 121 KDAIKKKLTGKHELOANCYEEVKDRCTLAELKGGSAVISLEGKPL 166
Db 121 KDAIKKKLTGKHELOANCYEEVKDRCTLAELKGGSAVISLEGKPL 166

RESULT 3
A29240
cofilin - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 28-Aug-1989 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C:Accession: A29240
R:Matsumoto, S.; Yahara, I.; Yonezawa, N.; Nishida, E.; Sakai, H.
J. Biol. Chem. 263, 11564-11566, 1988
A:Title: Cloning and characterization of porcine brain cofilin cDNA. Cofilin contains th
A:Reference number: A29240; MUID:88298817; PMID:3403546
A:Accession: A29240
A:Molecule type: mRNA
A:Residues: 1-166 <MAT>
A:Cross-references: UNIPROT:P10668; GB:M20866; NID:G164424; PIDN:AAA31020.1; PID:G164425
C:Comment: Cofilin reversibly regulates actin polymerization and depolymerization in a p
C:Superfamily: cofilin
C:Keywords: actin binding; phosphoprotein
F:26-36/Region: nuclear location signal
F:104-134/Region: actin binding #status predicted

Query Match 99.4%; Score 841; DB 1; Length 166;
Best Local Similarity 99.4%; Pred. No. 1.2e-60;
Matches 165; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MASGVAVSDGVKVFNDMKVRSSTPEEVKKRKAVALFCLSEDKNNIILEGKEILVGDV 60
Db 1 MASGVAVSDGVKVFNDMKVRSSTPEEVKKRKAVALFCLSEDKNNIILEGKEILVGDV 60

Qy 61 GQTVDDPYATFVKMLPKDCRYALYDITYETKESKEDLVFIWAPESAPLKSKMIYASS 120
Db 61 GQTVDDPYTFVKMLPKDCRYALYDITYETKESKEDLVFIWAPESAPLKSKMIYASS 120

Db 61 GQTVDDPYATFVKMLPKDCRYALYDITYETKESKEDLVFIWAPESAPLKSKMIYASS 120

Qy 121 KDAIKKKLTGKHELOANCYEEVKDRCTLAELKGGSAVISLEGKPL 166
Db 121 KDAIKKKLTGKHELOANCYEEVKDRCTLAELKGGSAVISLEGKPL 166

RESULT 4
S12584
cofilin - mouse
C:Species: Mus musculus (house mouse)
C:Date: 03-Feb-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C:Accession: S12584; JUI0201
R:Moriyama, K.; Matsumoto, S.; Nishida, E.; Sakai, H.; Yahara, I.
Nucleic Acids Res. 18, 3053, 1990
A:Title: Nucleotide sequence of mouse cofilin cDNA.
A:Reference number: S12584; MUID:90272419; PMID:2349104
A:Accession: S12584
A:Molecule type: mRNA
A:Residues: 1-166 <WOR>
A:Cross-references: UNIPROT:P18760; EMBL:D00472; NID:G220383; PIDN:BAA00364.1; PID:G2203
C:Comment: Cofilin reversibly regulates actin polymerization and depolymerization in a p
C:Superfamily: cofilin
C:Keywords: actin binding; phosphoprotein
F:26-36/Region: nuclear location signal
F:104-134/Region: actin binding #status predicted

Query Match 99.2%; Score 839; DB 1; Length 166;
Best Local Similarity 98.8%; Pred. No. 1.7e-60;
Matches 164; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MASGVAVSDGVKVFNDMKVRSSTPEEVKKRKAVALFCLSEDKNNIILEGKEILVGDV 60
Db 1 MASGVAVSDGVKVFNDMKVRSSTPEEVKKRKAVALFCLSEDKNNIILEGKEILVGDV 60

Qy 61 GQTVDDPYATFVKMLPKDCRYALYDITYETKESKEDLVFIWAPESAPLKSKMIYASS 120
Db 61 GQTVDDPYTFVKMLPKDCRYALYDITYETKESKEDLVFIWAPESAPLKSKMIYASS 120

Qy 121 KDAIKKKLTGKHELOANCYEEVKDRCTLAELKGGSAVISLEGKPL 166
Db 121 KDAIKKKLTGKHELOANCYEEVKDRCTLAELKGGSAVISLEGKPL 166

RESULT 5
A53812
cofilin, muscle - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C:Accession: A53812
R:Ono, S.; Minami, N.; Abe, H.; Obinata, T.
J. Biol. Chem. 269, 15280-15286, 1994
A:Title: Characterization of a novel cofilin isoform that is predominantly expressed in
A:Reference number: A53812; MUID:94253093; PMID:8195165
A:Accession: A53812
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-166 <ONO>
A:Cross-references: UNIPROT:P45591; GB:L29468; NID:G498016; PIDN:AAA37433.1; PID:G498017
C:Superfamily: cofilin
C:Keywords: actin binding; muscle

Query Match 83.0%; Score 702; DB 2; Length 166;
Best Local Similarity 81.3%; Pred. No. 1.8e-49;
Matches 135; Conservative 14; Mismatches 17; Indels 0; Gaps 0;

Qy 1 MASGVAVSDGVKVFNDMKVRSSTPEEVKKRKAVALFCLSEDKNNIILEGKEILVGDV 60
Db 1 MASGVAVSDGVKVFNDMKVRSSTPEEVKKRKAVALFCLSEDKNNIILEGKEILVGDV 60

Qy 61 GQTVDDPYATFVKMLPKDCRYALYDITYETKESKEDLVFIWAPESAPLKSKMIYASS 120
Db 61 GQTVDDPYTFVKMLPKDCRYALYDITYETKESKEDLVFIWAPESAPLKSKMIYASS 120

QY 121 KDAIKKLTGKIHQLQANCYEEVKDRTCTLAELKGGSAVISLEKPL 166
 DB 121 KDAIKKLTGKIHQLQANCYEEVKDRTCTLAELKGGSAVISLEKPL 166

RESULT 6
 B35703
 Cofillin - chicken
 C:Species: Gallus gallus (chicken)
 C>Date: 12-Oct-1990 #sequence_revision 27-Jun-1994 #text_change 22-Jun-1999
 C:Accession: B35703
 R:Abbe, H.; Endo, T.; Yamamoto, K.; Obinata, T.
 Biochemistry 29, 7420-7425, 1990
 A:Title: Sequence of cDNAs encoding actin depolymerizing factor and cofilin of embryonic chick brain
 A:Reference number: A35703; MUID:91027755; PMID:1699599
 A:Accession: B35703
 A:Molecule type: mRNA
 A:Residues: 1-166 <ABE>
 A:Cross-references: GB:M55659; NID:g211569; PIDN:AAAG2732.1; PID:g211570; GB:J02915
 C:Comment: Cofilin reversibly regulates actin polymerization and depolymerization in a phosphorylation-dependent manner
 C:Superfamily: cofilin
 C:Keywords: actin binding; phosphoprotein
 F:26-36/Region: actin binding; phosphoprotein
 F:104-134/Region: actin binding #status predicted

Query Match 82.9%; Score 701; DB 1; Length 166;
 Best Local Similarity 81.3%; Pred. No. 2.2e-49;
 Matches 135; Conservative 12; Mismatches 19; Indels 0; Gaps 0;

QY 1 MASGVAVSDGVIVKFNMDKVRKSSSTPEEVKKRKAVALFCLSEDKNIIIEEGKEILVGDV 60
 DB 1 MASGVAVSDGVIVKFNMDKVRKSSSTPEEVKKRKAVALFCLSEDKNIIIEEGKEILVGDV 60

QY 61 GOTVDDPYATFVKMLPDKDCRYALYDATTETKESKEDLVFIWAPESAPLKSMMIYASS 120
 DB 61 GOTVDDPYATFVKMLPDKDCRYALYDATTETKESKEDLVFIWAPESAPLKSMMIYASS 120

QY 121 KDAIKKLTGKIHQLQANCYEEVKDRTCTLAELKGGSAVISLEKPL 166
 DB 121 KDAIKKLTGKIHQLQANCYEEVKDRTCTLAELKGGSAVISLEKPL 166

RESULT 7
 A35702
 Destrin - chicken
 N:Alternate names: actin-depolymerizing factor
 C:Species: Gallus gallus (chicken)
 C>Date: 12-Oct-1990 #sequence_revision 05-Aug-1994 #text_change 09-Jul-2004
 C:Accession: A35702; A35703; A40672
 R:Adams, M.E.; Minamide, L.S.; Duester, G.; Bamberg, J.R.
 Biochemistry 29, 7414-7420, 1990
 A:Title: Nucleotide sequence and expression of a cDNA encoding chick brain actin depolymerizing factor
 A:Reference number: A35702; MUID:91027754; PMID:2223773
 A:Accession: A35702
 A:Molecule type: mRNA
 A:Residues: 1-165 <ADA>
 A:Cross-references: UNIPROT:P18359; GB:J02912; NID:g211096; PIDN:AAA48575.1; PID:g211097
 A:Experimental source: brain
 A>Note: part of this sequence was confirmed by peptide sequencing
 R:Abbe, H.; Endo, T.; Yamamoto, K.; Obinata, T.
 Biochemistry 29, 7420-7425, 1990
 A:Title: Sequence of cDNAs encoding actin depolymerizing factor and cofilin of embryonic chick brain
 A:Reference number: A35703; MUID:91027755; PMID:1699599
 A:Accession: A35703
 A:Molecule type: mRNA
 A:Residues: 1-165 <ABE>
 A:Cross-references: GB:M55660; GB:J02915; NID:g211092; PIDN:AAA48573.1; PID:g211093
 A:Experimental source: muscle
 A>Note: part of this sequence was confirmed by peptide sequencing
 R:Morgan, T.E.; Lockerbie, R.O.; Minamide, L.S.; Browning, M.D.; Bamberg, J.R.

J. Cell Biol. 122, 623-633, 1993
 A:Title: Isolation and characterization of a regulated form of actin depolymerizing factor
 A:Reference number: A40672; MUID:93328764; PMID:7687605
 A:Accession: A40672
 A:Molecule type: protein
 A:Residues: 20-30 <MOR>
 R:Agnew, B.J.; Minamide, L.S.; Bamberg, J.R.
 J. Biol. Chem. 270, 17582-17587, 1995
 A:Title: Reactivation of phosphorylated actin depolymerizing factor and identification of phosphorylation sites
 A:Reference number: A38989; MUID:95340558; PMID:7615564
 C:Contents: annotation; acetylated amino end; phosphorylation site
 C:Comment: Destrin is an actin-binding protein that is capable of rapidly depolymerizing actin
 C:Superfamily: cofilin
 C:Keywords: acetylated amino end; actin binding; phosphoprotein
 F:2-165/Product: Destrin #status predicted
 F:26-36/Region: nuclear location signal
 F:104-134/Region: actin binding #status predicted
 F:2/Modified site: acetylated amino end (Ala) (in mature form) #status experimental
 F:3/Binding site: phosphate (Ser) (covalent) #status experimental

Query Match 73.3%; Score 620.5; DB 1; Length 165;
 Best Local Similarity 73.5%; Pred. No. 6.3e-43;
 Matches 122; Conservative 18; Mismatches 25; Indels 1; Gaps 1;

QY 1 MASGVAVSDGVIVKFNMDKVRKSSSTPEEVKKRKAVALFCLSEDKNIIIEEGKEILVGDV 60
 DB 1 MASGVAVSDGVIVKFNMDKVRKSSSTPEEVKKRKAVALFCLSEDKNIIIEEGKEILVGDV 60

QY 61 GOTVDDPYATFVKMLPDKDCRYALYDATTETKESKEDLVFIWAPESAPLKSMMIYASS 120
 DB 61 GOTVDDPYATFVKMLPDKDCRYALYDATTETKESKEDLVFIWAPESAPLKSMMIYASS 120

QY 121 KDAIKKLTGKIHQLQANCYEEVKDRTCTLAELKGGSAVISLEKPL 166
 DB 121 KDAIKKLTGKIHQLQANCYEEVKDRTCTLAELKGGSAVISLEKPL 166

RESULT 8
 A35179
 Destrin - pig
 N:Alternate names: actin-depolymerizing factor
 C:Species: Sus scrofa domestica (domestic pig)
 C>Date: 03-Aug-1990 #sequence_revision 05-Aug-1994 #text_change 09-Jul-2004
 C:Accession: A35179
 R:Moriyama, K.; Nishida, E.; Yonezawa, N.; Sakai, H.; Matsumoto, S.; Iida, K.; Yahara, I.
 J. Biol. Chem. 265, 5768-5773, 1990
 A:Title: Destrin, a mammalian actin-depolymerizing protein, is closely related to cofilin
 A:Reference number: A35179; MUID:90202824; PMID:2156828
 A:Accession: A35179
 A:Molecule type: mRNA
 A:Residues: 1-165 <MOR>
 A:Cross-references: UNIPROT:P60982; GB:D90053; GB:J05290; NID:g217681; PIDN:BA414105.1; PID:g217682
 A:Experimental source: brain
 C:Comment: Destrin is an actin-binding protein that is capable of rapidly depolymerizing actin
 C:Superfamily: cofilin
 C:Keywords: acetylated amino end; actin binding; phosphoprotein
 F:2-165/Product: Destrin #status predicted
 F:26-36/Region: nuclear location signal
 F:104-134/Region: actin binding #status predicted
 F:2/Modified site: acetylated amino end (Ala) (in mature form) #status predicted
 F:3/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 71.7%; Score 606.5; DB 1; Length 165;
 Best Local Similarity 71.1%; Pred. No. 8.4e-42;
 Matches 118; Conservative 21; Mismatches 26; Indels 1; Gaps 1;

QY 1 MASGVAVSDGVIVKFNMDKVRKSSSTPEEVKKRKAVALFCLSEDKNIIIEEGKEILVGDV 60
 DB 1 MASGVAVSDGVIVKFNMDKVRKSSSTPEEVKKRKAVALFCLSEDKNIIIEEGKEILVGDV 60

QY 61 GOTVDDPYATFVKMLPDKDCRYALYDATTETKESKEDLVFIWAPESAPLKSMMIYASS 120
 DB 61 GOTVDDPYATFVKMLPDKDCRYALYDATTETKESKEDLVFIWAPESAPLKSMMIYASS 120

00 168817G191YAIJFSEVAIE-IVDEKV 134

DB 3 ASGMHVSDECKLKFLETK-----AKRNRYRFIVFKIDEKAQVVMIDK-----LGNPE 50

00 180017G191QAIJFSEVAIE-IVDEKV 134

Db 51 ETYED---FTRSIPEDECRYAVYDYFTIPENCQSKIFFIAWSPDTSRVRSKMLYASS 106
Qy 121 KDAIKKLTGKHELOANCYEE-----VKORCTL 149
Db 107 KDRFKRELDGIQVELQATDPSEMSLDIIKGRVNL 140

RESULT 15
G84717
actin depolymerizing factor 6 [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C/Accession: G84717
R/Lin. X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A/Reference number: A84420; MUID:20083487; PMID:10617197
A/Accession: G84717
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-132 <STO>
A/Cross-references: GB:AE002093; NID:g4432815; PIDN:AAD20665.1; GSPDB:GN00139
C/Genetics:
A/Gene: At2g31200
A/Map position: 2
C/Superfamily: cofilin

Query Match 24.6%; Score 208; DB 2; Length 132;
Best Local Similarity 35.7%; Pred. No. 7e-10;
Matches 41; Conservative 32; Mismatches 32; Indels 10; Gaps 3;
Qy 30 KRRKAVLFCLESDKKNIILEEGKEILVGDVGQTVDDPYATFVKLPDKDCRYALYDQY 89
Db 17 KKHRYVVFVKIDSKKEVVEK-----TGNPTESYDD---FLASLPDNDCRYAVYDFDF 67
Qy 90 ETKESKKEDLVFIF-WAPESAPLKSMMIYASSKDAIKKLTGKHELOANCYEEV 143
Db 68 VTSENCQSKIFFFAWSPSTSGIRAKVLYSTSKOOLSGRELQGIHYEQATDPTEV 122

Search completed: May 13, 2005, 09:47:33
Job time : 39 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 13, 2005, 09:29:44 ; Search time 176 Seconds
(without alignments)
482.984 Million cell updates/sec

Title: US-10-649-952A-1
Perfect score: 846
Sequence: 1 MASGAVSDGVKVFNDMKV.....CTLAELGGSAVISLEGKPL 166

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	841	99.4	165	1	COF1_HUMAN
2	837	98.9	165	1	COF1_RAT
3	836	98.8	165	1	COF1_PIG
4	836	98.8	165	1	COF1_SHEEP
5	834	98.6	165	1	COF1_MOUSE
6	831	98.2	229	2	Q9CX22
7	709	83.8	166	1	COF1_CHICK
8	702	83.0	166	1	COF2_MOUSE
9	699	82.6	166	1	COF2_HUMAN
10	693	81.9	166	2	Q6N2W3
11	659	77.9	168	2	Q6NX11
12	656	77.5	168	1	COF2_XENLA
13	649	76.7	168	1	COF1_XENLA
14	625.5	73.9	165	2	Q6TH32
15	615.5	72.8	164	1	DEST_CHICK
16	606.5	71.7	164	1	DEST_MOUSE
17	604.5	71.5	165	2	Q6DV06
18	601.5	71.1	164	1	DEST_HUMAN
19	601.5	71.1	164	1	DEST_PIG
20	598.5	70.7	164	2	Q7W0E3
21	392.5	46.4	163	2	Q7ZWD8
22	310.5	36.7	153	2	Q7ZXD4
23	282.5	33.4	153	2	Q6C0Y0
24	280	33.1	143	2	Q9HF97
25	276	32.6	143	2	Q6BWX4
26	273	32.3	143	2	Q6C022
27	271	32.0	143	2	Q759P0
28	268	31.7	143	2	Q96VU9
29	267.5	31.6	143	1	COF1_YEAST
30	265	31.3	143	2	Q6FV81
31	260	30.7	111	2	Q8N1B5

32	257.5	30.4	156	2	Q05307
33	257	30.4	137	1	ACTP_ACACA
34	254	30.0	137	1	COFI_SCHPO
35	230	27.2	137	1	COFI_DICDI
36	227.5	26.9	139	2	Q6T8D2
37	227	26.8	139	1	ADP3_MAIZE
38	224.5	26.5	146	2	Q8LCM6
39	222.5	26.3	463	2	Q6JAGO
40	220.5	26.1	139	1	ADFI_PETHY
41	220	26.0	140	2	Q9M594
42	219.5	25.9	139	1	ADFI_ARATH
43	219.5	25.9	143	1	ADP2_PETHY
44	217.5	25.7	139	1	ADP4_ARATH
45	216	25.5	139	2	Q84TB3

ALIGNMENTS

RESULT 1					
COFI_HUMAN					
ID	COFI_HUMAN	STANDARD;	PRT;	165	AA.
AC	P23528; Q9UCA2;				
DT	01-NOV-1991 (Rel. 20, Created)				
DT	25-JAN-2005 (Rel. 46, Last sequence update)				
DT	25-JAN-2005 (Rel. 46, Last annotation update)				
DE	Cofilin, non-muscle isoform (Cofilin-1) (18 kDa phosphoprotein) (p18).				
GN	Name=CFL1; Synonyms=CFL;				
OS	Homo sapiens (Human)				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Placenta;				
RX	MEDLINE=91088330; PubMed=2263493;				
RA	Ogawa K., Tashima M., Yumoto Y., Okuda T., Sawada H., Okuma M.,				
RA	Maruyama Y.;				
RT	"Coding sequence of human placenta cofilin cDNA.";				
RL	Nucleic Acids Res. 18:7169-7169(1990).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RA	der Steege G., Draaijers T.G., Grootsoorten P.M., Ozinga J.,				
RA	Anzeveno R., Velona I., Brahe C., Scheffer H., van Ommen G.J.B.,				
RA	Buyt C.H.C.M.;				
RL	Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=96393663; PubMed=8800436;				
RA	Gillett G.T., Fox M.F., Rowe P.S.N., Casimir C.M., Povey S.;				
RT	"Mapping of human non-muscle type cofilin (CFL1) to chromosome 11q13				
RT	and muscle-type cofilin (CFL2) to chromosome 14.";				
RL	Ann. Hum. Genet. 60:201-211(1996).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Lung, Ovary, Placenta, and Uterus;				
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;				
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,				
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,				
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,				
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,				
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,				
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,				
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,				
RA	Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,				
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,				
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,				
RA	Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,				
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,				
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,				
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,				
RA	Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,				

Q05307	saccharomyc
P37167	acanthamoeb
P78929	schizosacch
P54706	dictyosteli
Q6T8D2	helianthus
Q41764	zea mays (m
Q8LCM6	arabidopsis
Q6JAGO	sorghum bic
Q9FV12	petunia hyb
Q9M594	elaeis guin
Q39250	arabidopsis
Q9FV11	petunia hyb
Q9ZK3	arabidopsis
Q84TB3	oryza sativ

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RL and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 (5)
 RP SEQUENCE OF 1-20.
 RP TISSUE=Platelet;
 RC MEDLINE=22608298; PubMed=12665801; DOI=10.1038/nbt810;
 RX Davidson M.M., Haslam R.J.;
 RA Gevaert K., Goethals M., Martens L., Van Damme J., Staes A.,
 RA Thomas G.R., Vandekerckhove J.;
 RT "Exploring proteomes and analyzing protein processing by mass
 RT spectrometric identification of sorted N-terminal peptides";
 RL Nat. Biotechnol. 21:566-569 (2003).
 (6)
 RN SEQUENCE OF 51-70.
 RP TISSUE=Platelet;
 RC MEDLINE=94311852; PubMed=8037689;
 RX Davidson M.M., Haslam R.J.;
 RA "Dephosphorylation of cofilin in stimulated platelets: roles for a
 RT GTP-binding protein and Ca2+";
 RL Biochem. J. 301:41-47 (1994).
 CC -1- FUNCTION: Controls reversibly actin polymerization and
 CC depolymerization in a pH-sensitive manner. It has the ability to
 CC bind G- and F-actin in a 1:1 ratio of cofilin to actin. It is the
 CC major component of intranuclear and cytoplasmic actin rods.
 CC -1- SUBCELLULAR LOCATION: Intranuclear and cytoplasmic; almost
 CC completely in nucleus in cells exposed to heat shock or 10%
 CC dimethyl sulfoxide.
 CC -1- TISSUE SPECIFICITY: Widely distributed in various tissues.
 CC -1- PTM: The phosphorylation of Ser-23 may prevent recognition of the
 CC nuclear localization signal.
 CC -1- SIMILARITY: Belongs to the actin-binding proteins ADF family.
 CC
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 CC
 CC EMBL; D00682; BAA00589.1; -
 CC EMBL; U21909; AAA64501.1; -
 CC EMBL; X95404; CAA64685.1; -
 CC EMBL; BC011005; AAH11005.1; -
 CC EMBL; BC012285; AAH12285.1; -
 CC EMBL; BC012318; AAH12318.1; -
 CC EMBL; BC018256; AAH18256.1; -
 CC PIR; S12632; S12632.
 CC HSSP; P18282; IAK6.
 CC SWISS-2DPAGE; P23528; HUMAN.
 CC Aarhus/Ghent-2DPAGE; 4; IEF.
 CC OGP; P23528; -
 CC Genew; HGNC:1874; CFL1.
 CC H-InvDB; HIX0009808; -
 CC MIW; 601442; -
 CC GO; GO:0005634; C:nucleus; TAS.
 CC GO; GO:0030036; P:actin cytoskeleton organization and biogenesis; TAS.
 CC GO; GO:0007266; P:Rho protein signal transduction; TAS.
 CC InterPro; IPR002108; Actbind_cofin.
 CC Pfam; PF00241; Cofilin_ADF; 1.
 CC PRINTS; PR00006; COFILIN.
 CC ProDom; PD002129; Actbind_cofin; 1.
 CC SMART; SM00102; ADF; 1.
 CC PROSITE; PS00325; ACTIN DEPOLYMERIZING; 1.
 CC Actin-binding; Cytoskeleton; Direct protein sequencing;
 CC Nuclear protein; Phosphorylation.
 CC INIT MET 0
 CC 0
 CC DONA1N 29 33 Nuclear localization signal (Potential).
 CC DONA1N 105 124 Actin-binding (Potential).
 CC MOD RES 23 23 Phosphoserine (Probable).
 CC SEQUENCE 165 AA; 18371 MW; EC9251A6D1C7C84C CRC64;
 SQ

Query Match 99.4%; Score 841; DB 1; Length 165;
 Best Local Similarity 100.0%; Pred. No. 6.9e-62;
 Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 ASGVAVSDGVKVFNDMKVYKSSPTPEHVKKRKAIVLFCISDKKNIILEGKEILVGDVG 61
 DB 1 ASGVAVSDGVKVFNDMKVYKSSPTPEHVKKRKAIVLFCISDKKNIILEGKEILVGDVG 60
 QY 62 QTVDVDPVATFVKMLPKDKCRVYALDYATYETKSKKEDLVFIWAPESAPLKSMMIYASSK 121
 DB 61 QTVDVDPVATFVKMLPKDKCRVYALDYATYETKSKKEDLVFIWAPESAPLKSMMIYASSK 120
 QY 122 DAIKKLTGIKHELOANCYEEVKDRCTLAELGSSAVISLEGKPL 166
 DB 121 DAIKKLTGIKHELOANCYEEVKDRCTLAELGSSAVISLEGKPL 165
 RESULT 2
 COFI_RAT
 ID COFI_RAT STANDARD; PRT; 165 AA.
 AC P45592;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Cofilin, non-muscle isoform (Cofilin-1).
 GN Name=Cfil1;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=101116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar; TISSUE=Brain;
 RA Shirasawa T., Takahashi H., Sakanoto K., Kawashima A., Akashi T.;
 RL Submitted (OCT-1991) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE, ACETYLATION, PHOSPHORYLATION SITE SER-23, AND MASS
 RP SPECTROMETRY.
 RC TISSUE=Parotid gland;
 RA Kanamori T., Suzuki M.M., Titani K.;
 RT "Complete amino acid sequences and phosphorylation sites, determined
 RT by Edman degradation and mass spectrometry, of rat parotid destrin-and
 RT cofilin-like protein.";
 RL Submitted (AUG-1998) to the PIR data bank.
 CC -1- FUNCTION: Controls reversibly actin polymerization and
 CC depolymerization in a pH-sensitive manner. It has the ability to
 CC bind G- and F-actin in a 1:1 ratio of cofilin to actin. It is the
 CC major component of intranuclear and cytoplasmic actin rods (By
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Intranuclear and cytoplasmic (By
 CC similarity).
 CC -1- TISSUE SPECIFICITY: Widely distributed in various tissues (By
 CC similarity).
 CC -1- PTM: The phosphorylation of Ser-23 may prevent recognition of the
 CC nuclear localization signal.
 CC -1- SIMILARITY: Belongs to the actin-binding proteins ADF family.
 CC
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 CC
 CC EMBL; X62908; CAA44694.1; -
 CC PIR; S49101; S49101.
 CC HSSP; P18282; IAK6.
 CC RGD; 69285; Cfil1.
 CC InterPro; IPR002108; Actbind_cofin.
 CC Pfam; PF00241; Cofilin_ADF; 1.
 CC PRINTS; PR00006; COFILIN.
 CC ProDom; PD002129; Actbind_cofin; 1.

DR SMART; SM00102; ADF; 1.
 DR PROSITE; PS00325; ACTIN_DEPOLYMERIZING; 1.
 KW Acetylation; Actin-binding; Cytoskeleton; Direct protein sequencing;
 KW Nuclear protein; Phosphorylation.
 FT INIT MET 0 0
 FT MOD_RES 1 1 N-acetylalanine.
 FT DOMAIN 29 33 Nuclear localization signal (Potential).
 FT DOMAIN 105 124 Actin-binding (Potential).
 FT MOD_RES 23 23 Phosphoserine.
 SQ SEQUENCE 165 AA; AD8FFACB671CA5E7 CRC64;
 Query Match 98.9%; Score 837; DB 1; Length 165;
 Best Local Similarity 99.4%; Pred. No. 1.5e-61;
 Matches 164; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 ASGVAVSDGVKVFNDKMKVRSSTPEVKRKKAVLFCLSSEDKKNILLEGKEILVGDVG 61
 DB 1 ASGVAVSDGVKVFNDKMKVRSSTPEVKRKKAVLFCLSSEDKKNILLEGKEILVGDVG 60
 QY 62 QTVDPPYATFVKMLPKDCKRYALDYATYETKESKEDLVFIWAPESAPLKSMMIYASSK 121
 DB 61 QTVDPPYATFVKMLPKDCKRYALDYATYETKESKEDLVFIWAPESAPLKSMMIYASSK 120
 QY 122 DAIKKKLTGKHLEQANCYEEVKDRTLAELGSSAVISLEGKPL 166
 DB 121 DAIKKKLTGKHLEQANCYEEVKDRTLAELGSSAVISLEGKPL 165
 RESULT 3
 COPI_PIG
 ID COPI_PIG STANDARD; PRT; 165 AA.
 AC P10658; Q29374;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 25-JAN-2005 (Rel. 46, Last sequence update)
 DT 25-JAN-2005 (Rel. 46, Last annotation update)
 DE Cofilin, non-muscle isoform (Cofilin-1).
 GN Name=CFL1;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=88298817; PubMed=3403546;
 RA Matsuzaki F., Matsumoto S., Yahara I., Yonezawa N., Nishida E.,
 Sakai H.;
 RT "Cloning and characterization of porcine brain cofilin cDNA. Cofilin
 contains the nuclear transport signal sequence.";
 RL J. Biol. Chem. 263:11564-11568(1988).
 RN [2]
 RP SEQUENCE OF 1-103 FROM N.A.
 RC TISSUE=Small intestine;
 RX MEDLINE=96327607; PubMed=8672129;
 RA Winteroe A.K., Fredholm M., Davies W.;
 RT "Evaluation and characterization of a porcine small intestine cDNA
 library: analysis of 839 clones.";
 RL Mamm. Genome 7:509-517(1996).
 CC -!- FUNCTION: Controls reversibly actin polymerization and
 depolymerization in a pH-sensitive manner. It has the ability to
 bind G- and F-actin in a 1:1 ratio of cofilin to actin. It is the
 major component of intranuclear and cytoplasmic actin rods.
 CC -!- SUBCELLULAR LOCATION: Intranuclear and cytoplasmic; almost
 completely in nucleus in cells exposed to heat shock or 10%
 dimethyl sulfoxide.
 CC -!- TISSUE SPECIFICITY: Widely distributed in various tissues.
 CC -!- PTM: The phosphorylation of Ser-23 may prevent recognition of the
 nuclear localization signal.
 CC -!- MISCELLANEOUS: A double mutation of Lys-111 and Lys-113 to Gln
 produces a mutant with no ability to depolymerize or bind F-actin.
 CC -!- SIMILARITY: Belongs to the actin-binding proteins ADF family.
 CC -----
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 CC -----
 DR EMBL; M20866; AAA31020.1; -;
 DR EMBL; F14577; CAA23134.1; -;
 DR PIR; A29240; A29240.
 DR HSSP; P18282; LAK6.
 DR InterPro; IPR002108; Actbind cofln.
 DR Pfam; PF00241; Cofilin_ADF; 1.
 DR PRINTS; PR00006; COFILIN.
 DR ProDom; PD002129; Actbind_cofln; 1.
 DR SMART; SM00102; ADF; 1.
 DR PROSITE; PS00325; ACTIN_DEPOLYMERIZING; 1.
 KW Actin-binding; Cytoskeleton; Direct protein sequencing;
 KW Nuclear protein; Phosphorylation.
 FT INIT MET 0 0 By similarity.
 FT DOMAIN 29 33 Nuclear localization signal (Potential).
 FT DOMAIN 105 124 Actin-binding (Potential).
 FT MOD_RES 23 23 Phosphoserine (By similarity).
 FT MUTAGEN 111 111 K->Q: Slight modification of activity.
 FT MUTAGEN 113 113 K->Q: Impairs interaction with actin.
 SQ SEQUENCE 165 AA; 18387 MW; EC9241B6D1D7D84C CRC64;
 Query Match 98.8%; Score 836; DB 1; Length 165;
 Best Local Similarity 99.4%; Pred. No. 1.8e-61;
 Matches 164; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 ASGVAVSDGVKVFNDKMKVRSSTPEVKRKKAVLFCLSSEDKKNILLEGKEILVGDVG 61
 DB 1 ASGVAVSDGVKVFNDKMKVRSSTPEVKRKKAVLFCLSSEDKKNILLEGKEILVGDVG 60
 QY 62 QTVDPPYATFVKMLPKDCKRYALDYATYETKESKEDLVFIWAPESAPLKSMMIYASSK 121
 DB 61 QTVDPPYATFVKMLPKDCKRYALDYATYETKESKEDLVFIWAPESAPLKSMMIYASSK 120
 QY 122 DAIKKKLTGKHLEQANCYEEVKDRTLAELGSSAVISLEGKPL 166
 DB 121 DAIKKKLTGKHLEQANCYEEVKDRTLAELGSSAVISLEGKPL 165
 RESULT 4
 COPI_SHEEP
 ID COPI_SHEEP STANDARD; PRT; 165 AA.
 AC Q6B7M7;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-JAN-2005 (Rel. 46, Last sequence update)
 DT 25-JAN-2005 (Rel. 46, Last annotation update)
 DE Cofilin, non-muscle isoform (Cofilin-1).
 GN Name=CFL1;
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Endometrium;
 RA Welker J.E., Ott T.L.;
 RT "Cloning and characterization of cofilin-1 expression in cyclic and
 early pregnant ovine endometrium following isolation by yeast-two
 hybrid screening.";
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Controls reversibly actin polymerization and
 depolymerization in a pH-sensitive manner. It has the ability to
 bind G- and F-actin in a 1:1 ratio of cofilin to actin. It is the
 major component of intranuclear and cytoplasmic actin rods (By
 similarity).
 CC -!- SUBCELLULAR LOCATION: Intranuclear and cytoplasmic (By
 similarity).

CC -1- PTM: The phosphorylation of Ser-23 may prevent recognition of the
 CC nuclear localization signal (By similarity).
 CC -1- SIMILARITY: Belongs to the actin-binding proteins ADP family.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; AY676116; AAT77679.1; -
 CC ProDom; PD002129; Actbind coflin; 1.
 CC PROSITE; PS00325; ACTIN DEPOLYMERIZING; 1.
 CC Actin-binding; Cytoskeleton; Nuclear protein; Phosphorylation.
 CC INIT MET 0 By similarity.
 CC DOMAIN 29 33 Nuclear localization signal (Potential).
 CC FT DOMAIN 105 124 Actin-binding (Potential).
 CC FT MOD RES 23 23 Phosphoserine (By similarity).
 CC SQ SEQUENCE 165 AA; 18387 MW; EC9241B6D1D7D84C CRC64;
 CC
 CC Query Match 98.8%; Score 836; DB 1; Length 165;
 CC Best Local Similarity 99.4%; Pred. No. 1.8e-61;
 CC Matches 164; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 CC
 CC QY 2 ASGVAVSDGVTKVFNMDKVRKSSPEEVKKKKAVLFCLESDKKNIILEGKELVGDVG 61
 CC Db 1 ASGVAVSDGVTKVFNMDKVRKSSPEEVKKKKAVLFCLESDKKNIILEGKELVGDVG 60
 CC
 CC QY 62 QTVDVDPYATFVKMLPKDCKRYALYDATYETKESKEDLVFIWAPESAPLKSMMIYASSK 121
 CC Db 61 QTVDVDPYATFVKMLPKDCKRYALYDATYETKESKEDLVFIWAPESAPLKSMMIYASSK 120
 CC
 CC QY 122 DAIKKKLTGKHELOQANCYEEVKDRCCTLAELKGGSAVISLEGKPL 166
 CC Db 121 DAIKKKLTGKHELOQANCYEEVKDRCCTLAELKGGSAVISLEGKPL 165
 CC
 CC RESULT 5
 CC COFI_MOUSE STANDARD; PRT; 165 AA.
 CC AC P18760;
 CC DT 01-NOV-1990 (Rel. 16, Created)
 CC DT 25-JAN-2005 (Rel. 46, Last sequence update)
 CC DT 25-JAN-2005 (Rel. 46, Last annotation update)
 CC DE Cofilin, non-muscle isoform (Cofilin-1).
 CC GN Name=Cfli1;
 CC OS Mus musculus (Mouse).
 CC OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC OX NCBI_TaxID=10090;
 CC (1)
 CC RN SEQUENCE FROM N.A.
 CC RP STRAIN=Swiss Webster;
 CC RC MEDLINE=90272419; PubMed=2349104;
 CC RX Moriyama K., Matsunoto S., Nishida E., Sakai H., Yahara I.;
 CC RA "Nucleotide sequence of mouse cofilin cDNA";
 CC RL Nucleic Acids Res. 18:3053-3053(1990).
 CC (2)
 CC RN SEQUENCE FROM N.A.
 CC RP STRAIN=C57BL/6; TISSUE=Brain;
 CC RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 CC RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 CC RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 CC RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 CC RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 CC RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 CC RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 CC RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 CC RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullah S.J.,
 CC RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 CC RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: Controls reversibly actin polymerization and
 CC depolymerization in a pH-sensitive manner. It has the ability to
 CC bind G- and F-actin in a 1:1 ratio of cofilin to actin. It is the
 CC major component of intranuclear and cytoplasmic actin rods.
 CC -1- SUBCELLULAR LOCATION: Intranuclear and cytoplasmic; almost
 CC completely in nucleus in cells exposed to heat shock or 10%
 CC dimethyl sulfoxide.
 CC -1- TISSUE SPECIFICITY: Widely distributed in various tissues.
 CC -1- PTM: The phosphorylation of Ser-23 may prevent recognition of the
 CC nuclear localization signal.
 CC -1- SIMILARITY: Belongs to the actin-binding proteins ADP family.
 CC
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 CC
 CC EMBL; D00472; BAA00364.1; -
 CC EMBL; BC058726; AAH58726.1; -
 CC PIR; S12584; S12584.
 CC HSP; P18282; IAK6.
 CC DR SWISS-2DPAGE; P18760; MOUSE.
 CC DR MGD; MGI:101757; Cfli1.
 CC DR InterPro; IPR002108; Actbind coflin.
 CC DR Pfam; PF00241; Cofilin ADP; 1.
 CC DR PRINTS; PR00006; COFILIN.
 CC DR ProDom; PD002129; Actbind coflin; 1.
 CC DR PROSITE; PS00325; ACTIN DEPOLYMERIZING; 1.
 CC KW Actin-binding; Cytoskeleton; Nuclear protein; Phosphorylation.
 CC FT INIT MET 0 By similarity.
 CC FT DOMAIN 29 33 Nuclear localization signal (Potential).
 CC FT DOMAIN 105 124 Actin-binding (Potential).
 CC FT MOD RES 23 23 Phosphoserine (By similarity).
 CC SQ SEQUENCE 165 AA; 18428 MW; AD8FE7D66701B8E7 CRC64;
 CC
 CC Query Match 98.6%; Score 834; DB 1; Length 165;
 CC Best Local Similarity 98.8%; Pred. No. 2.6e-61;
 CC Matches 163; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 CC
 CC QY 2 ASGVAVSDGVTKVFNMDKVRKSSPEEVKKKKAVLFCLESDKKNIILEGKELVGDVG 61
 CC Db 1 ASGVAVSDGVTKVFNMDKVRKSSPEEVKKKKAVLFCLESDKKNIILEGKELVGDVG 60
 CC
 CC QY 62 QTVDVDPYATFVKMLPKDCKRYALYDATYETKESKEDLVFIWAPESAPLKSMMIYASSK 121
 CC Db 61 QTVDVDPYATFVKMLPKDCKRYALYDATYETKESKEDLVFIWAPESAPLKSMMIYASSK 120
 CC
 CC QY 122 DAIKKKLTGKHELOQANCYEEVKDRCCTLAELKGGSAVISLEGKPL 166
 CC Db 121 DAIKKKLTGKHELOQANCYEEVKDRCCTLAELKGGSAVISLEGKPL 165
 CC
 CC RESULT 6
 CC COFX_MOUSE PRELIMINARY; PRT; 229 AA.
 CC ID Q9CX22
 CC AC Q9CX22; 2001 (TrEMBLrel. 17, Created)
 CC DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 CC DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 CC DE Mus musculus 12 days embryo embryonic body between diaphragm region

DE and neck cDNA, RIKEN full-length enriched library, clone:94300600J01
DE product:cotfilin 1, non-muscle, full insert sequence.
GN Name=Cfil1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RC TISSUE=Embryonic body between diaphragm region and neck;
RX MEDLINE=92279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RC TISSUE=Embryonic body between diaphragm region and neck;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RC TISSUE=Embryonic body between diaphragm region and neck;
RA The FANTOM Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RC TISSUE=Embryonic body between diaphragm region and neck;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RC TISSUE=Embryonic body between diaphragm region and neck;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RC TISSUE=Embryonic body between diaphragm region and neck;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai K., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Taya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AK020471; BAB32114.1; -.
DR HSP; P60982; 1AK6.
DR MGD; MGI:101757; Cfil1.
DR GO; GO:0030864; C:cortical actin cytoskeleton; IDA.
DR InterPro; IPR002108; Actbind_cofin.
DR Pfam; PF00241; Cofilin_ADF; I.
DR PRINTS; PR00006; COFILIN.
DR ProDom; PD002129; Actbind_cofin; 1.
DR SMART; SM00102; ADF; 1.
DR PROSITE; PS00325; ACTIN DEPOLYMERIZING; 1.
SQ SEQUENCE 229 AA; 24735 MW; 1198EAA68F166B75 CRC64;
Query Match 98.2%; Score 831; DB 2; Length 229;
Best Local Similarity 98.2%; Pred. No. 6.8e-61;
Matches 162; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 MASGVAVSDGVIVKVFNDMKVRKSTPEEVKKRKAVALFCLSEDKKNILLEGKEILVGDV 60
DB 1 MASGVAVSDGVIVKVFNDMKVRKSTPEEVKKRKAVALFCLSEDKKNILLEGKEILVGDV 60
QY 61 GQTVDDPYATFVKMLPDKCRVALYDATTETKSKKEDLVFIWAPESAPLKSVMYASS 120
DB 61 GQTVDDPYATFVKMLPDKCRVALYDATTETKSKKEDLVFIWAPENAPLKSVMYASS 120
QY 121 KDAIKKLTGIRKHELQANCYEEVKDRTLAELGGSVAVISLEGP 165
DB 121 KDAIKKLTGIRKHELQANCYEEVKDRTLAELGGSVAVISLEGP 165
RESULT 7
COFI_CHICK STANDARD; PRT; 166 AA.
ID ID COFI_CHICK STANDARD; PRT; 166 AA.
AC AC P21566;
DT 01-MAY-1991 (Rel. 18, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cofilin.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=91027755; PubMed=1699599;
RA Abe H., Endo T., Yamamoto K., Obinata T.;
RT "Sequence of cDNAs encoding actin depolymerizing factor and cofilin of
RT embryonic chicken skeletal muscle: two functionally distinct actin-
RL regulatory proteins exhibit high structural homology.";
RL Biochemistry 29:7420-7425(1990).
RN [2]
RP STRUCTURE BY NMR, AND REVISIONS TO 53-54.
RX MEDLINE=21880669; PubMed=11885570; DOI=10.1023/A:1014227808686;
RA Bains N.P.S., Gorbatyuk V.Y., Nosworthy N.J., Robson S.A.,
RA Mactejewski M.W., dos Remedios C.G., King G.F.;
RT "Backbone and side-chain 1H, 15N, and 13C assignments for chick
RT cofilin.";
RL J. Biomol. NMR 22:193-194(2002).
CC -!- FUNCTION: Controls reversibly actin polymerization and
CC depolymerization in a pH-sensitive manner. It has the ability to
CC bind G- and F-actin in a 1:1 ratio of cofilin to actin. It is the
CC major component of intranuclear and cytoplasmic actin rods.
CC -!- SUBCELLULAR LOCATION: Intranuclear and cytoplasmic; almost
CC completely in nucleus in cells exposed to heat shock or 10%
CC dimethyl sulfoxide.
CC -!- TISSUE SPECIFICITY: Widely distributed in various tissues.
CC -!- PTM: The phosphorylation of Ser-24 may prevent recognition of the
CC nuclear localization signal.
CC -!- SIMILARITY: Belongs to the actin-binding proteins ADF family.
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 CC -----

DR EMBL; M55659; AAA62732.1; --
 DR HSP; P18282; IAK6
 DR InterPro; IPR002108; Actbind_coflin.
 DR Pfam; PF00241; Cofilin_ADF; 1.
 DR PRINTS; PR00006; COFILIN.
 DR ProDom; PD002129; Actbind_coflin; 1.
 DR SMART; SM00102; ADF; 1.
 DR PROSITE; PS00325; ACTIN DEPOLYMERIZING; 1.
 KW Actin-binding; Cytoskeleton; Nuclear protein; Phosphorylation.
 FT DOMAIN 30 34 Nuclear localization signal (Potential).
 FT DOMAIN 106 125 Actin-binding (Potential).
 FT MOD RES 24 24 Phosphoserine (By similarity).
 SQ SEQUENCE 166 AA; 18661 MW; 514685E940786EFO CRC64;

Query Match 83.8%; Score 709; DB 1; Length 166;
 Best Local Similarity 81.9%; Pred. No. 6e-51;
 Matches 136; Conservative 13; Mismatches 17; Indels 0; Gaps 0;

Qy 1 MASGVAVSDGVIKVFNDMKVRSSTPEVKRKKAVLFCLSDDKNIILLEGKEILVGDV 60
 Db 1 MASGVTNDEVKIVFNDMKVRSSTPEVKRKKAVLFCLSDDKNIILLEGKEILVGDV 60
 Qy 61 GQTVDDPYATFVKMLPKDKCRYALYDITYETKESKEDLVFIWAPESAPLKSQMIYASS 120
 Db 61 GQTVDDPYATFVKMLPKDKCRYALYDITYETKESKEDLVFIWAPESAPLKSQMIYASS 120
 Qy 121 KDAIKKLTGKHLEQANCYEEVKDRCTLAELKGGSAVISLEGKPL 166
 Db 121 KDAIKKLTGKHLEQANCYEEVKDRCTLAELKGGSAVISLEGKPL 166

RESULT 8

ID COF2_MOUSE STANDARD; PRT; 166 AA.
 AC P45591;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Cofilin, muscle isoform (Cofilin-2).
 GN Name=Cfl2;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C3H; TISSUE=Skeletal muscle;
 RX MEDLINE=94253093; PubMed=8195165;
 RA Ono S., Winami N., Abe H., Obinata T.;
 RT "Characterization of a novel cofilin isoform that is predominantly
 RL expressed in mammalian skeletal muscle.";
 RN J. Biol. Chem. 269:15280-15286(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: Controls reversibly actin polymerization and
 CC depolymerization in a pH-sensitive manner. It has the ability to
 CC bind G- and F-actin in a 1:1 ratio of cofilin to actin. It is the
 CC major component of intranuclear and cytoplasmic actin rods.
 CC -1- SUBCELLULAR LOCATION: Intranuclear and cytoplasmic.
 CC -1- TISSUE SPECIFICITY: Predominantly expressed in skeletal muscle.
 CC -1- PM: The phosphorylation of Ser-24 may prevent recognition of the
 CC nuclear localization signal.
 CC -1- SIMILARITY: Belongs to the actin-binding proteins ADF family.
 CC -----

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DR EMBL; L29468; AAA37433.1; --
 DR EMBL; BC007138; AAH07138.1; --
 DR PIR; A53812; A53812.
 DR HSP; P18282; IAK6.
 DR MGI; MGI:101763; Cf12.
 DR InterPro; IPR002108; Actbind_coflin.
 DR Pfam; PF00241; Cofilin_ADF; 1.
 DR PRINTS; PR00006; COFILIN.
 DR ProDom; PD002129; Actbind_coflin; 1.
 DR SMART; SM00102; ADF; 1.
 DR PROSITE; PS00325; ACTIN DEPOLYMERIZING; 1.
 KW Actin-binding; Cytoskeleton; Nuclear protein; Phosphorylation.
 FT DOMAIN 30 34 Nuclear localization signal (Potential).
 FT DOMAIN 106 125 Actin-binding (Potential).
 FT MOD RES 24 24 Phosphoserine (By similarity).
 SQ SEQUENCE 166 AA; 18709 MW; 48B6D7E5AE9FE1CC CRC64;

Query Match 83.0%; Score 702; DB 1; Length 166;
 Best Local Similarity 81.3%; Pred. No. 2.3e-50;
 Matches 135; Conservative 14; Mismatches 17; Indels 0; Gaps 0;

Qy 1 MASGVAVSDGVIKVFNDMKVRSSTPEVKRKKAVLFCLSDDKNIILLEGKEILVGDV 60
 Db 1 MASGVTNDEVKIVFNDMKVRSSTPEVKRKKAVLFCLSDDKNIILLEGKEILVGDV 60
 Qy 61 GQTVDDPYATFVKMLPKDKCRYALYDITYETKESKEDLVFIWAPESAPLKSQMIYASS 120
 Db 61 GQTVDDPYATFVKMLPKDKCRYALYDITYETKESKEDLVFIWAPESAPLKSQMIYASS 120
 Qy 121 KDAIKKLTGKHLEQANCYEEVKDRCTLAELKGGSAVISLEGKPL 166
 Db 121 KDAIKKLTGKHLEQANCYEEVKDRCTLAELKGGSAVISLEGKPL 166

RESULT 9

ID COF2_HUMAN STANDARD; PRT; 166 AA.
 AC Q9Y281;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Cofilin, muscle isoform (Cofilin-2).
 GN Name=Cfl2;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;

RN SEQUENCE FROM N.A.
 RA Jin J., Li G., Hu S., Li W., Yuan J., Qiang B.,
 RT "Isolation of two isoforms of human cofillin cDNA."
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=21315834; PubMed=11422377;
 RA Thirion C., Stucka R., Mendel B., Gruhler A., Jaksch M., Nowak K.J.,
 RA Binz N., Laing N.G., Lochmuller H.,
 RT "Characterization of human muscle type cofillin (CFL2) in normal and
 regenerating muscle."
 RL Eur. J. Biochem. 268:3473-3482(2001).
 [3]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Bone marrow, Placenta, and Skeletal muscle;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Casavant T.L., Scheetz T.E.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rubin G.M., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -I- FUNCTION: Controls reversibly actin polymerization and
 depolymerization in a pH-sensitive manner. It has the ability to
 bind G- and F-actin in a 1:1 ratio of cofillin to actin. It is the
 major component of intranuclear and cytoplasmic actin rods (by
 similarity).
 CC -I- SUBCELLULAR LOCATION: Intranuclear and cytoplasmic (by
 similarity).
 CC -I- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Comment=isoforms are identical at the level of the protein
 sequence;
 CC Name=CFL2b;
 CC IsoId=Q9Y281-1; Sequence=Displayed;
 CC Name=CFL2a;
 CC IsoId=Q9Y281-2; Sequence=Not described;
 CC -I- TISSUE SPECIFICITY: Isoform CFL2b is expressed predominantly in
 skeletal muscle and heart, while isoform CFL2a is expressed in
 various tissues.
 CC -I- PTM: The phosphorylation of Ser-24 may prevent recognition of the
 nuclear localization signal.
 CC -I- SIMILARITY: Belongs to the actin-binding proteins ADF family.
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF134802; AAD31280.1; -
 DR EMBL; AF134803; AAD31281.1; -
 DR EMBL; AF283513; AAF97934.1; -
 DR EMBL; AF242229; AAF64498.1; -
 DR EMBL; BC011444; AAH1444.1; -
 DR EMBL; BC022364; AAH22364.1; -

DR EMBL; BC022876; AAH22876.1; -
 DR HSSP; P18282; 1AKG.
 DR Genew; HGNC:1875; CFL2.
 DR MIM; 601443; -
 DR InterPro: IPR002108; Actbind cofln.
 DR Pfam; PF00241; Cofilin_ADF; 1.
 DR PRINTS; PRO0006; COFILIN.
 DR ProDom; PD002129; Actbind_cofln; 1.
 DR SMART; SM00102; ADF; 1.
 DR PROSITE; PS00325; ACTIN_DEPOLYMERIZING; 1.
 KW Actin-binding; Alternative splicing; Cytoskeleton; Nuclear protein;
 KW Phosphorylation.
 FT DOMAIN 30 34 Nuclear localization signal (Potential).
 FT DOMAIN 106 125 Actin-binding (Potential).
 FT MOD RES 24 24 Phosphoserine (By similarity).
 SQ SEQUENCE 166 AA; 18736 MW; 48B6CDA9FE1CC CRC64;
 Query Match 82.6%; Score 699; DB 1; Length 166;
 Best Local Similarity 80.7%; Pred. No. 4e-50;
 Matches 134; Conservative 15; Mismatches 17; Indels 0; Gaps 0;
 QY 1 MASGVAVSDGVKVFNDMKVRKSTPEEVKKKAVLFCLSDDKKNILLEGKEILVGDV 60
 DB 1 MASGVTVNDEVKVFNDMKVRKSTQEEIKKKKAVLFCLSDDKROIIVVEAKQLVGD 60
 QY 61 GOTVDDPYATFVKMLPDKCRVALYDATYETKESKEDLVFIWAPESAPLKSMTIYSS 120
 DB 61 GDTVEDPYTSFKLLPLNDCRYALYDATYETKESKEDLVFIWAPESAPLKSMTIYSS 120
 QY 121 KDAIKKLTGTHKELOANCYEEVKRCTLAEKLGSAVLSLEGKPL 166
 DB 121 KDAIKKKFTGIXHEWQVNLDDIKDRSTLGEKLGNNVVVLSLEGKPL 166
 RESULT 10
 Q6NZW3 PRELIMINARY; PRT; 166 AA.
 AC Q6NZW3;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE Cofilin 2 (Muscle).
 GN Name=cfl2;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Casavant T.L., Scheetz T.E.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rubin G.M., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

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RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Gerhard D.S.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC065947; AAH65947.1; -.
DR HSSP; P60982; IAK6.
DR ZFIN; ZDB-GENE-040426-1815; cfl2.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003779; F:actin binding; IEA.
DR InterPro; IPR002108; Actbind_cofin.
DR Pfam; PF00241; Cofilin_ADF; 1.
DR PRINTS; PR00006; COFILIN.
DR ProDom; PD002129; Actbind_cofin; 1.
DR SMART; SM00102; ADF; 1.
DR PROSITE; PS00325; ACTIN_DEPOLYMERIZING; 1.
SQ SEQUENCE 166 AA; 18560 MW; 795942E0F8F0A2D6 CRC64;

Query Match 81.9%; Score 693; DB 2; Length 166;
Best Local Similarity 80.1%; Pred. No. 1.3e-49;
Matches 133; Conservative 16; Mismatches 17; Indels 0; Gaps 0;

Qy 1 MASGVAVSDGVIVKVFNDKVRKSTPEEVKRRKKAVALFCLSEDKNKNIILEGKEILVGDV 60
Db 1 MASGTVSDGVIVKVFNDKVRKSSDEVKRRKKAVALFCLSDDKKKIIVEEGRIIVGDI 60

Qy 61 GQTVDDPYATFVKMLPKDCRYALYDATTYETKESKEDLVFIWAPESAPLKSKMIYASS 120
Db 61 GDSVDDPYATFVKMLPKDCRYALYDATTYETKESKEDLVFIWAPESAPLKSKMIYASS 120

Qy 121 KDAIKKKLTGKHQLQANCYEEVDRCTLAELGGSVAIVSLEKPL 166
Db 121 KDAIKKKFTGKHQWQVNGLLDIDQDSTLAELGGSVAIVSLEGRPL 166

RESULT 11
Q6NX11 PRELIMINARY; PRT; 168 AA.
AC Q6NX11;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein MGC76274.
GN Name=MGC76274;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=83364;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477933; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Narusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Frange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Kzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences."
RN [2] Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
```

```
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Gerhard D.S.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC067328; AAH67328.1; -.
DR HSSP; P60982; IAK6.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003779; F:actin binding; IEA.
DR InterPro; IPR002108; Actbind_cofin.
DR Pfam; PF00241; Cofilin_ADF; 1.
DR PRINTS; PR00006; COFILIN.
DR ProDom; PD002129; Actbind_cofin; 1.
DR SMART; SM00102; ADF; 1.
DR PROSITE; PS00325; ACTIN_DEPOLYMERIZING; 1.
SQ SEQUENCE 168 AA; 19073 MW; 14AB09FF9616496A CRC64;

Query Match 77.9%; Score 659; DB 2; Length 168;
Best Local Similarity 78.3%; Pred. No. 8.4e-47;
Matches 130; Conservative 8; Mismatches 28; Indels 0; Gaps 0;

Qy 1 MASGVAVSDGVIVKVFNDKVRKSTPEEVKRRKKAVALFCLSEDKNKNIILEGKEILVGDV 60
Db 1 MASGVAVSDGVIVKVFNDKVRKSTPEEVKRRKKAVALFCLSEDKNKNIILEGKEILVGDV 60

Qy 61 GQTVDDPYATFVKMLPKDCRYALYDATTYETKESKEDLVFIWAPESAPLKSKMIYASS 120
Db 61 GQTVDDPYATFVKMLPKDCRYALYDATTYETKESKEDLVFIWAPESAPLKSKMIYASS 120

Qy 121 KDAIKKKLTGKHQLQANCYEEVDRCTLAELGGSVAIVSLEKPL 166
Db 121 KDAIKKKFTGKHQWQVNGLLDIDQDSTLAELGGSVAIVSLEGRPL 166

RESULT 12
Q6F2_XENLA STANDARD; PRT; 168 AA.
AC P45593;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cofilin 2.
GN Name=XAC2;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8335;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96180281; PubMed=8603919; DOI=10.1083/jcb.132.5.871;
RA Abe H., Ohtani T., Minamide L.S., Bamberg J.R.;
RT "Xenopus laevis actin-depolymerizing factor/cofilin: a
RT phosphorylation-regulated protein essential for development.";
RN [2] J. Cell Biol. 132:871-885(1996).
RP SEQUENCE FROM N.A.
RC TISSUE=Oocyte;
RA Wada A., Gotoh Y., Nishida E.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: Controls reversibly actin polymerization and
CC depolymerization in a pH-sensitive manner. It has the ability to
CC bind G- and F-actin in a 1:1 ratio of cofilin to actin. It is the
CC major component of intranuclear and cytoplasmic actin rods (By
CC similarity).
CC -I- SUBCELLULAR LOCATION: Intranuclear and cytoplasmic (By
CC similarity).
CC -I- SIMILARITY: Belongs to the actin-binding proteins ADF family.
CC
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DR	EMBL; U26269; BAB00539.1; -.	
DR	EMBL; D38406; BAA07461.1; -.	
DR	HSSP; P18282; IAK6.	
DR	InterPro; IPR002108; Actbind_cofln.	
DR	Pfam; PF00241; Cofilin_ADF; 1.	
DR	PRINTS; PR00006; COFILIN.	
DR	ProDom; PD002129; Actbind_cofln; 1.	
DR	SMART; SM00102; ADF; 1.	
DR	PROSITE; PS00345; ACTIN DEPOLYMERIZING; 1.	
KW	Actin-binding; Cytoskeleton; Nuclear protein; Phosphorylation.	
FT	DOMAIN 30 34	
FT	DOMAIN 106 125	
FT	SEQUENCE 168 AA; 19120 MW; 6DBCE7F8397EDFD1 CRC64;	
FT	SEQUENCE 168 AA; 19120 MW; 6DBCE7F8397EDFD1 CRC64;	

Query Match	77.5%	Score 656;	DB 1;	Length 168;
Best Local Similarity	75.3%;	Pred. No. 1.5e-46;		
Matches 125;	Conservative 15;	Mismatches 26;	Indels 0;	Gaps 0;
Qy	1	MASGVAVSDGVKVFENDMKVRKSGSTPEEVKVRKKAVALFCLSDOKNIIILEGGKEILGVDV	60	
Db	1	MASGVWSDDVVKVFENDMKVRKHQUSPEAKRKRKAVIFCLSDOKKTIILPGKEILQGVDV	60	
Qy	61	GQTVDDPYATFVRMLPDKDCRYALDYATYETKESKEDLVFIWFAPESAPLKSMMIYASS	120	
Db	61	GCNVDPYKTFVRMLPRLDRCRYALDYALYETKTKEDLVFVFWAPEASLKSMMIYASS	120	
Qy	121	KDAIKKLTGIIKHELQANCYEEVKDRCTLAEKLGGSVAVISLEKPL	166	
Db	121	KDAIRKRFTGIIKEHWQNTYDNDNDPCNLADKLGSGNTVWSLEKSL	166	

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RESULT 13
COPI_XENLA STANDARD; PRT; 168 AA.
ID COPI_XENLA
AC P45695;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cofilin 1.
GN Names=XAC1;
OS Xenopus laevis (African clawed frog).
OC Amphibia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=96180281; PubMed=8603919; DOI=10.1083/jcb.132.5.871;
RX Abe H., Obinata T., Minamide L.S., Bamberg J.R.;
RT "Xenopus laevis actin-dpolymerizing factor/cofilin: a
RT phosphorylation-regulated protein essential for development.";
RL J. Cell Biol. 132:871-885(1996).
CC -1- FUNCTION: Controls reversibly actin polymerization and
CC depolymerization in a pH-sensitive manner. It has the ability to
CC bind G- and F-actin in a 1:1 ratio of cofilin to actin. It is the
CC major component of intranuclear and cytoplasmic actin rods (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Intranuclear and cytoplasmic (By
CC similarity).
CC -1- SIMILARITY: Belongs to the actin-binding proteins ADF family.
CC
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CC

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DR ENBL; U26270; AAB00540.1; -.
DR HSSP; P18282; 1AK6.
DR InterPro; IPR002108; Actbind_cofln.
DR Pfam; PF00241; Cofilin_ADF; 1.
DR PRINTS; PR00006; COFILIN.
DR ProDom; PD002129; Actbind_cofln; 1.
DR SMART; SM00102; ADF; 1.
DR PROSITE; PS00325; ACTIN DEPOLYMERIZING; 1.
DR Actin-binding; Cytokeleton; Nuclear localization; Phosphorylation.
FW FT DOMAIN 30 34 Nuclear localization signal (Potential).
FT FT DOMAIN 106 125 Actin-binding (Potential).
SQ SEQUENCE 168 AA; 19066 MW; F3A4D8635A3683D6 CRC64;

Query Match 76.7%; Score 649; DB 1; Length 168;
Best Local Similarity 76.2%; Pred. No. 5.7e-46;
Matches 125; Conservative 14; Mismatches 25; Indels 0; Gaps 0

Qy 1 MASGVAVSDGVIKVFNDMKVRKSTPTEVKKRKKAVLFCLESDKNTILLEGKEILVGDV 60
Db 1 MASGVVSDDVTKVFENKMKVRHQJSPEDAKRKKAVVFCLESDDKTKTILLEGKEILQGD 60
Qy 61 GTQVDDPYATFVKMLPDKCRYALYDATYETKSKKEDLVFIWPESAPLKSMTYASS 120
Db 61 GCNVEDPYTKFVKMLPRNDCRYALDYALYETKTKEDLVFVFWAPEASLKSMTYASS 120
Qy 121 KDAIKKKLTGKHGLQANCYEEVVDKRCITLAEKGGGSAVISLEGK 164
Db 121 KDAIKKRLPGIKHEWQINTYEDVNDPCNLADKLGCGTWSLEGK 164

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RESULT 14
Q6TH32 PRELIMINARY; PRT; 165 AA.
ID
AC Q6TH32;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Muscle coflin 2.
GN Name=cfl21; Synonyms=CFL2;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_TaxID=7955;
RN [1]
SEQUENCE FROM N.A.
RP TISSUE=Kidney marrow.
RC Song H.D., Wu X.Y., Sun X.J., Zhou Y., Liu T.X., Deng M., Zhang G.W.,
RA Sheng Y., Chen Y., Ruan Z., Jiang C.L., Fan H.Y., Zou L.I.,
RA Kanki J.P., Look A.T., Chen Z.
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY398324; AAQ97757.1; -.
DR HSSP: P60982; IAK6.
DR ZFIN: ZDB-GENE-030131-215; cfl21.
DR GO: GO:0005622; C:intracellular; IEA.
DR GO: GO:0003779; F:actin binding; IEA.
DR InterPro: IPR002108; Actbind coflin.
DR Pfam: PF00241; Coflin_ADF; I.
DR PRINTS: PR00006; COFLIN.
DR Prodom: PD002129; Actbind_coflin; 1.
DR SMART: SM00102; ADF; 1.
DR PROSITE: PS00325; ACTIN DEPOLYMERIZING; 1.
SQ SEQUENCE 165 AA; 18717 MW; 3FD3F8F542E2A707 CRC64;

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Query Match      73.9%; Score 625.5; DB 2; Length 165;
Best Local Similarity 74.9%; Pred. No. 4.9e-44;
Matches 125; Conservative 17; Mismatches 20; Indels 5; Gaps 2

QY 1 MASGVAVSDGVKVPNDMKVKRSTPBEVK-KRKQAVLFCLSDKKNIILEGKEKILVGD 59
      ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 1 MASGVVTEETVLTVFNEMKVRKARHCNEEEKSKKKAVMFCLSDDKKHIIIMEQGQEILOD 60
      ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

QY 60 VGSOTVDDDPVATFVKMLPDKCRVYALDYATYETKESKKEDLVFIFWAPEAPLKSMMIYAS 119

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Db 61 EG-----DPLKFKVQMLPNDCRYALYDATYETKTKEDLVFIWAPESAPLKSMMIYAS 116
Qy 120 SKDAIKKKLTGKIKHELQANCVEEVKDRCTLAELGGSAVISLEGKPL 166
Db 117 SKDAIKKKKFTGKIKHEWQVNGMDIKDRKTLAELGGASVVSLEGKPL 163

RESULT 15
ID DEST CHICK STANDARD; PRT; 164 AA.
AC P18359;
DT 01-NOV-1990 (Rel. 16, Created)
DT 25-JAN-2005 (Rel. 46, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Destrin (Actin-depolymerizing factor) (ADF).
GN Name=DSTN; Synonyms=DSN;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RN SEQUENCE FROM N.A., AND SEQUENCE OF 100-110 AND 115-133.
RP TISSUE=Brain;
RX MEDLINE=91027754; PubMed=2223773;
RA Adams M.E., Minamide L.S., Duester G., Bamberg J.R.;
RT "Nucleotide sequence and expression of a cDNA encoding chick brain
actin depolymerizing factor.";
RL Biochemistry 29:7414-7420(1990).
RN [2]
RN SEQUENCE FROM N.A.
RP TISSUE=Skeletal muscle;
RX MEDLINE=91027755; PubMed=1699599;
RA Abe H., Endo T., Yamamoto K., Obinata T.;
RT "Sequence of cDNAs encoding actin depolymerizing factor and cofilin of
embryonic chicken skeletal muscle: two functionally distinct actin-
regulatory proteins exhibit high structural homology.";
RL Biochemistry 29:7420-7425(1990).
CC -1- FUNCTION: Actin-depolymerizing protein. Severs actin filaments (F-
actin) and binds to actin monomers (G-actin). Acts in a pH-
independent manner.
CC -1- SIMILARITY: Belongs to the actin-binding proteins ADF family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J02912; AAA48575.1; -.
DR EMBL; M55660; AAA48573.1; -.
DR PIR; A35702; A35702.
DR HSSP; P18282; 1AK6.
DR InterPro; IPR002108; Actbind_cofln.
DR Pfam; PF00241; Cofilin_ADF; 1.
DR PRINTS; PR00006; COFILIN.
DR ProDom; PD002129; Actbind_cofln; 1.
DR SMART; SM00102; ADF; 1.
DR PROSITE; PS00325; ACTIN DEPOLYMERIZING; 1.
KW Actin-binding; Direct protein sequencing.
FT INIT_MET 0 By similarity.
FT DOMAIN 29 33 Nuclear localization signal (Potential).
FT DOMAIN 105 124 Actin-binding (Potential).
SQ SEQUENCE 164 AA; 18401 MW; 72747A1D43E6E3E9 CRC64;
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Query Match 72.8%; Score 615.5; DB 1; Length 164;
Best Local Similarity 73.3%; Pred. No. 3.3e-43;
Matches 121; Conservative 18; Mismatches 25; Indels 1; Gaps 1;
Qy 2 ASGVAVSDGVIKFVNDKVRKSTPEVKRKKAVLFCLSRDKKNIILEGKILVGDVG 61
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Db 1 ASGVQVADVEYCRIFYDMKVRKCSIPREVKRKKAVIFCLSPDKKCIIVEGKEILVGDVG 60
Qy 62 QTVDPPYATFVRKMLPKDKCRYALYDATYETKESKKEDLVFIWAPESAPLKSMMIYASSK 121
Db 61 VTTVPFKHFVEMLPKDKCRYALYDASFETKESKKBELMFLWAPEQAPLKSMMIYASSK 120
Qy 122 DAIKKKLTGKIKHELQANCVEEVKDRCTLAELGGSAVISLEGKPL 166
Db 121 DAIKKKFQGIKHECQANGPEDLNRAK--IAEKJGGSLVVAFGSPV 164
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Search completed: May 13, 2005, 09:46:49
Job time : 178 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 13, 2005, 09:38:50 ; Search time 43 Seconds
(without alignments)
288.180 Million cell updates/sec

Title: US-10-649-952A-1
Perfect score: 846
Sequence: 1 MASGVAVSGVVKVFNMDKV.....CTLAELGGSVISLEGGKPL 166

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A COMB.pdp.*
- 2: /cgn2_6/ptodata/1/iaa/5B COMB.pdp.*
- 3: /cgn2_6/ptodata/1/iaa/6A COMB.pdp.*
- 4: /cgn2_6/ptodata/1/iaa/6B COMB.pdp.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pdp.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pdp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	616	72.8	127	4	US-09-513-999C-8059
2	606.5	71.7	185	4	US-09-513-999C-7957
3	354	41.8	86	4	US-09-513-999C-5489
4	287	33.9	69	4	US-09-513-999C-5488
5	242.5	28.7	146	4	US-09-513-999C-20627
6	188.5	22.3	154	4	US-09-248-796A-20627
7	149	17.6	30	1	US-08-184-252A-5
8	149	17.6	30	5	PCT-US95-00601-5
9	124	14.7	28	4	US-09-017-689A-4
10	124	14.7	30	1	US-08-184-252A-6
11	124	14.7	30	5	PCT-US95-00601-6
12	120	14.2	350	2	US-09-123-851-3
13	120	14.2	350	2	US-08-728-520-3
14	116	13.7	350	1	US-08-184-252A-2
15	116	13.7	350	5	PCT-US95-00601-2
16	101.5	12.0	141	2	US-08-187-186A-5
17	100	11.8	123	4	US-09-248-796A-15632
18	100	11.8	353	4	US-09-270-767-42030
19	98.5	11.6	343	2	US-09-123-851-1
20	98.5	11.6	343	2	US-08-728-520-1
21	96.5	11.4	141	2	US-08-442-497C-9
22	96.5	11.4	141	3	US-09-333-033-9
23	96.5	11.4	141	4	US-10-004-832-9
24	96.5	11.4	137	4	US-09-949-016-7648
25	92.5	10.9	303	4	US-09-248-796A-21504
26	91	10.8	30	1	US-08-184-252A-7
27	91	10.8	30	5	PCT-US95-00601-7

28	87.5	10.3	646	4	US-09-543-681A-6840	Sequence 6840, Ap
29	86.5	10.2	228	4	US-09-248-796A-20501	Sequence 20501, A
30	86	10.2	391	4	US-09-543-681A-7029	Sequence 7029, Ap
31	84	9.9	116	4	US-09-513-999C-8034	Sequence 8034, Ap
32	82.5	9.8	142	2	US-08-187-186A-2	Sequence 2, Appli
33	82.5	9.8	142	2	US-08-442-497C-2	Sequence 2, Appli
34	82.5	9.8	142	3	US-09-333-033-2	Sequence 2, Appli
35	82.5	9.8	142	4	US-10-004-832-2	Sequence 2, Appli
36	82.5	9.8	142	5	PCT-US94-05186-2	Sequence 2, Appli
37	82.5	9.8	143	4	US-09-949-016-11009	Sequence 11009, A
38	81.5	9.6	142	4	US-09-663-600A-229	Sequence 229, App
39	81.5	9.6	476	4	US-09-051-961-8	Sequence 8, Appli
40	81.5	9.6	2862	4	US-09-595-684B-31	Sequence 31, Appli
41	81.5	9.6	2663	4	US-09-538-092-1252	Sequence 1252, Ap
42	80.5	9.5	430	4	US-09-107-532A-5101	Sequence 5101, Ap
43	80	9.5	1007	4	US-09-538-092-736	Sequence 736, App
44	79.5	9.4	161	4	US-09-248-796A-15514	Sequence 15514, A
45	79.5	9.4	2733	4	US-09-949-016-11433	Sequence 11433, A

ALIGNMENTS

RESULT 1
US-09-513-999C-8059
; Sequence 8059, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclet, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59 US2 REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 8059
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 122
; OTHER INFORMATION: Xaa=Ala or Thr
US-09-513-999C-8059

Query Match	72.8%	Score	616	DB	4	Length	127
Best Local Similarity	100.0%	Pred.	No.	3.1e-62			
Matches	121	Conservative	0	Mismatches	0	Indels	0
						Gaps	0
Qy	1	MASGVAVSGVVKVFNMDKVRKSSSTPEEVKRRKAVLFCLSSEDKKNIILEEGKEILVGDV	60				
Db	1	MASGVAVSGVVKVFNMDKVRKSSSTPEEVKRRKAVLFCLSSEDKKNIILEEGKEILVGDV	60				
Qy	61	GQTVDPPVATFYKMLPDKDCRYALDYATYETKESKEDLVFIWAPESAPLKSMMIYASS	120				
Db	61	GQTVDPPVATFYKMLPDKDCRYALDYATYETKESKEDLVFIWAPESAPLKSMMIYASS	120				
Qy	121	K	121				
Db	121	K	121				

RESULT 2
US-09-513-999C-7957
; Sequence 7957, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.


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; APPLICANT: AVERBACK, Paul
; TITLE OF INVENTION: PHARMACEUTICALLY ACTIVE AGENTS THAT
; IMPEDE THE FORMATION OF AMYLOID BY IMPEDING THE GENESIS OF
; DMS
;
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/017,689A
; FILING DATE: 03-Feb-1998
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/038,694
; FILING DATE: 07-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 018792/0125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
;
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-017-689A--4
;
; Query Match 14.7%; Score 124; DB 4; Length 28;
; Best Local Similarity 96.0%; Pred. No. 3.4e-07;
; Matches 24; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
;
Qy 46 NIILEGKEILVGVGQTVDDPYAT 70
Db 1 NIILEGKDILVGVGQTVDDPYAT 25
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; RESULT 10
; Sequence 6, Application US/08184252A
; Patent No. 5573935
; GENERAL INFORMATION:
; APPLICANT: Beeler, John F.
; APPLICANT: LaRoche, William
; APPLICANT: Aaronson, Stuart A.
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE A6
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens Olson & Bear
; STREET: 620 Newport Center Drive, Sixteenth Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/08/184,252A
; FILING DATE: 18-JAN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned A.
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH084.001A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
US-08-184-252A-6
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; Query Match 14.7%; Score 124; DB 1; Length 30;
; Best Local Similarity 73.3%; Pred. No. 3.7e-07;
; Matches 22; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
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Qy 101 FIWAPESAPLKSMIYVASSKDAIKKLTG 130
Db 1 FIWAPDSAPIKSKMMYMTSTKDSIKKLVG 30
;
; RESULT 11
; PCT-US95-00601-6
; Sequence 6, Application PC/TUS9500601
; GENERAL INFORMATION:
; APPLICANT: United States of America Department of Health and Human
; APPLICANT: Services
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE A6
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens Olson & Bear
; STREET: 620 Newport Center Drive, Sixteenth Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00601
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned A.
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH084.001A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
PCT-US95-00601-6
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Query Match 14.7%; Score 124; DB 5; Length 30;
Best Local Similarity 73.3%; Pred. No. 3.7e-07;
Matches 22; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 101 FIFWAPESAPLKSMMIYASSKDAIKKLTG 130
Db 1 FILWAPDSAPIKSKMMYTSTKOSIRKLVG 30

RESULT 12

US-09-123-851-3
; Sequence 3, Application US/09123851
; Patent No. 5958405
; GENERAL INFORMATION:
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: A NOVEL HUMAN PROTEIN TYROSINE KINASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09123,851
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/728,520
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0136 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 451482

US-09-123-851-3
Query Match 14.2%; Score 120; DB 2; Length 350;
Best Local Similarity 27.0%; Pred. No. 3.6e-05;
Matches 34; Conservative 36; Mismatches 40; Indels 16; Gaps 6;

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Db 11 EDVKE-----IFARANGKRYLLKISIEHQVLVIGSYQSPDSWDKYDSFVLPLEDKQ 65

QY 80 CRYALYDATYETKESKEDLVFIWAPESAPLKSMMIYASSKDAIKKLTG--IKHELQA 137
Db 66 PCYILF--RLDSQNAQGYEWIFIAWSPDHSVHRQKMLYAATRAATLKKEFGGHIKDEVFG 123

QY 138 NCYEEV 143

Db 124 TVKEDV 129

RESULT 13

US-08-728-520-3
; Sequence 3, Application US/08728520
; Patent No. 5994112
; GENERAL INFORMATION:
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: A NOVEL HUMAN PROTEIN TYROSINE KINASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,520
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0136 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 451482

US-08-728-520-3
Query Match 14.2%; Score 120; DB 2; Length 350;
Best Local Similarity 27.0%; Pred. No. 3.6e-05;
Matches 34; Conservative 36; Mismatches 40; Indels 16; Gaps 6;

QY 27 BEVKRRKKAFLCLSEDKKNHILE---EGKEILVGVGQ---TVDDPYATFV-KMLPDKD 79
Db 11 EDVKE-----IFARANGKRYLLKISIEHQVLVIGSYQSPDSWDKYDSFVLPLEDKQ 65

QY 80 CRYALYDATYETKESKEDLVFIWAPESAPLKSMMIYASSKDAIKKLTG--IKHELQA 137
Db 66 PCYILF--RLDSQNAQGYEWIFIAWSPDHSVHRQKMLYAATRAATLKKEFGGHIKDEVFG 123

QY 138 NCYEEV 143

Db 124 TVKEDV 129

RESULT 14

US-08-184-252A-2
; Sequence 2, Application US/08184252A
; Patent No. 5573935
; GENERAL INFORMATION:
; APPLICANT: Beeler, John F.
; APPLICANT: LaRoche, William
; APPLICANT: Aaronson, Stuart A.
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE A6
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens Olson & Bear

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

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(without alignments)
3326.471 Million cell updates/sec

Title: US-10-649-952A-2

Perfect score: 901

Sequence: 1 atggctccggtgtggtgtg.....tggaggcgaagcctttgtga 501

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: : 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=A_Geneseq -QMT=fastan -SUFFIX=n2p.rag -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
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-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
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-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- 1: Geneseq16Dec04:*
- 2: Geneseq1980s:*
- 3: Geneseq1990s:*
- 4: Geneseq2000s:*
- 5: Geneseq2001s:*
- 6: Geneseq2002s:*
- 7: Geneseq2003as:*
- 8: Geneseq2003bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	846	93.9	166	5	ABBB1882
2	846	93.9	166	6	ADA37012 Human cof
3	846	93.9	166	8	ADI24535 Human mod
4	846	93.9	166	8	ADO05889 Human cof
5	846	93.9	166	8	ADQ30534 Pancreas
6	846	93.9	229	8	ADQ65133 Novel hum
7	842	93.5	187	6	ABR41637 Human DIT
8	841	93.3	239	8	ADN99790 Novel hum
9	764	84.8	149	7	Adj70464 Human hea
10	702	77.9	166	6	ABR41956 Mouse cof

11	699	77.6	166	4	AAM78545	Aam78545 Human pro
12	699	77.6	166	7	ADB75248	ADB75248 Prostate
13	699	77.6	166	7	ADJ70104	Adj70104 Human hea
14	699	77.6	166	8	ADI24536	ADI24536 Human mod
15	699	77.6	205	4	AAU18546	Aau18546 Human cyt
16	699	77.6	207	4	AAM79529	Aam79529 Human pro
17	666.5	74.0	154	8	ADN99460	Adn99460 Novel hum
18	645.5	71.6	153	8	ADN99430	Adn99430 Novel hum
19	628	69.7	127	3	AGQ30378	Agq30378 Human sec
20	606.5	67.3	165	3	AAG03876	Aag03876 Human sec
21	606.5	67.3	165	4	AAM40267	Aam40267 Human pol
22	606.5	67.3	165	8	ADI24537	ADI24537 Human mod
23	606.5	67.3	165	8	ADQ30570	Adq30570 Pancreas
24	606.5	67.3	165	8	ADP23096	Adp23096 PRO polyp
25	606.5	67.3	188	4	AAM42053	Aam42053 Human pol
26	581.5	64.5	170	8	ADI24538	ADI24538 Human mod
27	562.5	62.4	180	8	ADI24539	ADI24539 Human mod
28	557.5	61.9	148	7	ADJ70545	Adj70545 Human hea
29	520.5	57.8	111	7	ADE15627	Ade15627 Human str
30	460	51.1	129	4	AAU18547	Aau18547 Human cyt
31	450	49.9	156	4	AAU18521	Aau18521 Human cyt
32	426	47.3	144	8	ADI24541	ADI24541 Human mod
33	402.5	44.7	131	8	ADP30110	Adp30110 Human sec
34	401.5	44.6	136	8	ADI24540	ADI24540 Human mod
35	393.5	43.7	106	8	ADN99385	Adn99385 Novel hum
36	390	43.3	110	8	ADN99316	Adn99316 Novel hum
37	390	43.3	110	8	ADP30004	Adp30004 Human sec
38	374	41.5	209	4	ABG20129	Abg20129 Novel hum
39	354	39.3	86	3	AAG01408	Aag01408 Human sec
40	287	31.9	69	3	AAG01407	Aag01407 Human sec
41	273	30.3	106	5	ADP43208	Adp43208 Human ova
42	267.5	29.7	143	8	ADS43863	Ads43863 Bacterial
43	253.5	28.1	141	8	ADN12253	Adn12253 C. albica
44	245.5	27.2	141	8	ADN12255	Adn12255 C. albica
45	230	25.5	60	8	ABO56473	Abo56473 Human gen

ALIGNMENTS

RESULT 1

ABBB1882
ID ABBB1882 standard; protein; 166 AA.

XX ABBB1882;
AC ABBB1882;
DT 23-SEP-2002 (first entry)
XX Human cofilin 1 (non-muscle).
DE Human cofilin 1 (non-muscle).
XX Human; cofilin 1; CFL1; gene therapy; antisense gene therapy;
KW immunological disorder.
XX Homo sapiens.
OS Homo sapiens.
XX WO200194376-A1.
PN WO200194376-A1.
XX 13-DEC-2001.
PD 13-DEC-2001.
XX 11-JUN-2001; 2001WO-US018815.
PF 11-JUN-2001; 2001WO-US018815.
XX 09-JUN-2000; 2000US-0210884P.
PR 09-JUN-2000; 2000US-0210884P.
XX (GENA-) GENAISSANCE PHARM INC.
PA Anastasio AE, Duda A, Klien SE, Koshy B, Sausker EA;
PI WPI; 2002-566437/60.
XX N-PSDB; ABQ88640, ABQ88641.
DR Novel genetic variants of human cofilin 1, CFL1 gene for studying
PT expression, function of the gene and expressing CFL1 protein useful in
PT identifying drugs to treat immunological disorders.
XX

PS Disclosure; Fig 3; 84pp; English.

XX CC The invention relates to a novel polynucleotide sequence which is a
 CC polymorphic variant of a reference sequence for the cofillin 1 (non-
 CC muscle) (CFL1) gene or its fragment, or a polymorphic variant of a
 CC reference sequence for a CFL1 cDNA or its fragment. The polynucleotide of
 CC the invention may have a use in gene therapy, and in antisense gene
 CC therapy. The polynucleotide is useful for studying the expression and
 CC function of CFL1 and expressing CFL1 protein for use in screening for
 CC candidate drugs to treat diseases related to CFL1 activity. The
 CC polymorphism and haplotype data are useful for validating whether CFL1 is
 CC a suitable target for drugs to treat immunological disorders, screening
 CC for such drugs and reducing bias in clinical trials of such drugs. The
 CC present sequence represents the human cofillin 1 (non-muscle) of the
 CC invention

XX SQ Sequence 166 AA;

Alignment Scores:
 Pred. No.: 1,43e-82 Length: 166
 Score: 846.00 Matches: 166
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 93.90% Indels: 0
 DB: 5 Gaps: 0

US-10-649-952A-2 (1-501) x ABB81882 (1-166)

Qy 1 ATGCGCTCCGTTGGCTGCTCTGATGTTCTCAAGGTTTCAACGACATGAAGTG 60
 Db 1 MetAlaSerGlyValAlaValSerAspGlyValIleLysValPheAsnAspMetLysVal 20
 Qy 61 CGTAAGCTTCAACGCCAGAGGCTGAGAGCGGAGAGGCGGCTCTCTCGCTG 120
 Db 21 ArgLysSerSerThrProGluGluValLysLysLysLysLysLysLysLysLysLysLys 40
 Qy 121 AGTGAGGACAAAGAAACATCATCTGAGGAGGCGGAGGAGATCTCTGGGCGATGTG 180
 Db 41 SerGluAspLysLysAsnIleLeuGluGluGluGluGluGluGluGluGluGluGluGluGlu 60
 Qy 181 GGCAGACTGTCGACGATCCCTACGCCACCTTTGTCAGATGTCGCCAGATAAGGACTGC 240
 Db 61 GlyGlnThrValAspAspProTyrAlaThrPheValLysMetLeuProAspLysAspCys 80
 Qy 241 CGCTATGCTCTATGATGCAACCTATCAGACCAAGGAGGAGGAGGAGGATCTCGTG 300
 Db 81 ArgTyrAlaLeuTyrAspAlaThrTyrGluThrLysGluSerLysLysGluAspLeuVal 100
 Qy 301 TTTATCTTCTGGGCCCCGAGTCTGCGCCCCCTTAAGAGCAAAATGATTATGCCAGCTCC 360
 Db 101 PheIlePheTrpAlaProGluSerAlaProLeuLysSerLysMetIleTyrAlaSerSer 120
 Qy 361 AAGGAGCCATCAAGAGAAGCTGACAGGGATCAAGCATGAATTGCAAGCAAACTGTAC 420
 Db 121 LysAspAlaIleLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 140
 Qy 421 GAGGAGTCAAGGACCGCTGACCGCTGCAGAGAGCTGGGGGACGTGGCTCATCTCC 480
 Db 141 GluGluValLysAspArgCysThrLeuAlaGluLysLysLysLysLysLysLysLysLysLys 160
 Qy 481 CTGGAGGCGAAGCCTTTG 498
 Db 161 LeuGluGlyLysProLeu 166

RESULT 2

ADA37012
 ID ADA37012 standard; protein; 166 AA.

XX CC ADA37012;
 AC
 XX 20-NOV-2003 (first entry)
 DT
 XX Human cofillin protein SEQ ID NO:1.
 DE

XX KW proliferation; differentiation; haematopoietic stem cell; cofilin;
 KW vasotrophic; antianemic; cytostatic; vulnary; nephrotropic;
 KW hepatotropic; haematopoietic hypofunction; Fanconi's disease;
 KW malignant lymphoma; acute leukaemia; chronic hepatic obstruction;
 KW kidney failure; surgical trauma; transfusion trauma; infection;
 KW snakebite; haemorrhagic uraemia; splenomegaly; Barnard-Soulier disease;
 KW Glanzmann's thrombasthenia; idiopathic thrombocytopenic purpura; human.
 XX OS Homo sapiens.
 XX WO2003057241-A1.
 XX 17-JUL-2003.
 XX 27-DEC-2002; 2002WO-JP013862.
 XX 28-DEC-2001; 2001JP-00400330.
 XX (DAII-) DAIICHI SUNTORY PHARMA CO LTD.
 XX (SUNR) SUNTORY LTD.
 XX (DAII-) DAIICHI SUNTORY BIOMEDICAL RES LTD.
 XX Miura K, Haruyama M, Kodama S;
 XX WPI; 2003-587077/55.
 XX N-PSDB; ADA37013.
 XX Agents containing cofilin promoting proliferation and differentiation of
 XX haematopoietic stem cells and their precursors for treatment of
 XX haematopoietic deficiency diseases.
 XX Claim 2; Fig 1; 57pp; Japanese.
 XX The present invention describes agents (A) promoting the proliferation
 XX and/or differentiation of haematopoietic stem cells and/or their
 XX precursor cells. (A) contain cofilin or a peptide of similar activity as
 XX active component. Also described: (1) promoting the proliferation and/or
 XX differentiation of haematopoietic stem cells and/or their precursor
 XX cells, using (A); and (2) treating diseases associated with
 XX haematopoietic cell deficiency, using (A). (A) have vasotropic,
 XX antianemic, cytostatic, vulnary, nephrotropic and hepatotropic
 XX activities. (A) can be used for treating and preventing diseases
 XX associated with a diffuse decrease in haematopoietic cell numbers and/or
 XX haematopoietic hypofunction, such as Fanconi's disease, malignant
 XX lymphoma, acute leukaemia, chronic hepatic obstruction, kidney failure,
 XX surgical or transfusion trauma, serious infections, snakebite,
 XX haemorrhagic uraemia, splenomegaly, Barnard-Soulier disease, Glanzmann's
 XX thrombasthenia, and idiopathic thrombocytopenic purpura. The present
 XX sequence represents human cofilin, which is given in the exemplification
 XX of the present invention.

SQ Sequence 166 AA;

Alignment Scores:
 Pred. No.: 1,43e-82 Length: 166
 Score: 846.00 Matches: 166
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 93.90% Indels: 0
 DB: 5 Gaps: 0

US-10-649-952A-2 (1-501) x ADA37012 (1-166)

Qy 1 ATGCGCTCCGTTGGCTGCTCTGATGTTCTCAAGGTTTCAACGACATGAAGTG 60
 Db 1 MetAlaSerGlyValAlaValSerAspGlyValIleLysValPheAsnAspMetLysVal 20
 Qy 61 CGTAAGCTTCAACGCCAGAGGCTGAGAGCGGAGAGGCGGCTCTCTCGCTG 120
 Db 21 ArgLysSerSerThrProGluGluValLysLysLysLysLysLysLysLysLysLysLys 40
 Qy 121 AGTGAGGACAAAGAAACATCATCTGAGGAGGCGGAGGAGATCTCTGGTGGCGATGTG 180

Db 41 SerGluAspLysLysAsnIleLeuGluGluGlyLysGluIleLeuValGlyAspVal 60
 QY 181 GGCCAGACTGTCAGCAGCTCCTACGCCACCTTTGTCAAGATGCTGCCAGATAAGGACTGC 240
 Db 61 GlyGlnThrValAspAspProTyrAlaThrPheValLysMetLeuProAspLysAspCys 80
 QY 241 CGTATGCTCTATGATGCACTATGAGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
 Db 81 ArgTyrAlaLeuTyrAspAlaThrTyrGluThrLysSerLysLysGluAspLeuVal 100
 QY 301 TTTATCTTCTGGCCCGCCAGTCTGCCCTTAAAGAGCAAAATGATTTATGCGACTCC 360
 Db 101 PheIlePheTrpAlaProGluSerAlaProLeuLysSerLysMetIleTyrAlaSerSer 120
 QY 361 AAGGAGCCCATCAAGAGAGCTCAGGAGATCAAGGATCAAGTGAATGCAAGCAAACTGCTAC 420
 Db 121 LysAspAlaIleLysLysLysLeuThrGlyIleHisGluLeuGlnAlaAsnCysTyr 140
 QY 421 GAGGAGTCAAGACCGCTGACCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
 Db 141 GluGluValLysAspArgCysThrLeuAlaGluLysLeuGlyGlySerAlaValIleSer 160
 QY 481 CTGGAGGCAAGCCTTTG 498
 Db 161 LeuGluGlyLysProLeu 166
 RESULT 3
 AD124535
 ID AD124535 standard; protein; 166 AA.
 AC AD124535;
 DT
 XX
 DE Human modifier of Chk1 (MCHK) protein SEQ ID NO:85.
 XX
 KW Chk1 pathway modulating agent; modifier of Chk1; MCHK; cytostatic;
 KW gene therapy; cancer; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2004004785-A1.
 XX
 PD 15-JAN-2004.
 XX
 PF 09-JUL-2003; 2003WO-US021379.
 XX
 PR 10-JUL-2002; 2002US-0394845P.
 PR 16-SEP-2002; 2002US-0410986P.
 XX
 PA (EXEL-) EXELIXIS INC.
 XX
 PI Francis-Lang H, Roche S, Joo DM, Nicoll M, Hai B, Zhang H;
 PI Lickteig K, Amundsen CD, Jin Y, Adamkewicz JI, Platt DM;
 PI Hammonds RG;
 XX
 DR WPI: 2004-083465/08.
 DR N-PSDB; AD124485.
 XX
 PT Identifying a candidate Chk1 pathway modulating agent for treating e.g.,
 PT cancer, comprises contacting an assay system comprising a MCHK
 PT polypeptide or nucleic acid with a test agent and detecting a test agent-
 PT biased activity.
 XX
 PS Example; SEQ ID NO 85; 266pp; English.
 XX
 CC The present invention describes a method for identifying a candidate Chk1
 CC pathway modulating agent. The method comprises: (a) providing an assay
 CC system comprising a modifier of Chk1 (MCHK) polypeptide or nucleic acid;
 CC (b) contacting the system with a test agent, where the system provides a
 CC reference activity except in the presence of the test agent; and (c)
 CC detecting a test agent-biased activity, and a difference between the test

CC agent-biased activity and the reference activity. Also described: (1) a
 CC method for modulating Chk1 pathway of a cell; (2) a method for modulating
 CC Chk1 pathway in a mammalian cell; and (3) a method for diagnosing a
 CC disease in a patient. A MCHK sequence has cytostatic activity, and can be
 CC used in gene therapy. The method is useful for identifying a candidate
 CC Chk1 pathway-modulating agent for preparing a composition for diagnosing
 CC or treating e.g., cancer. The present sequence represents a human MCHK
 CC protein, which is used in the exemplification of the present invention.
 XX
 SQ Sequence 166 AA;
 Alignment Scores:
 Pred. No.: 1,43e-82 Length: 166
 Score: 846.00 Matches: 166
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 93.90% Indels: 0
 DB: 8 Gaps: 0
 US-10-649-952A-2 (1-501) x AD124535 (1-166)
 QY 1 ATGGCCCTCCGGTGTGGCTGCTCTGATGCTCATCAAGGTGTTCAACGACATGAAGGTG 60
 Db 1 MetAlaSerGlyValAlaValSerAspGlyValIleLysValPheAsnAspMetLysVal 20
 QY 61 CGTAAGTCTTCAACGCCAGAGAGGTGAAGAAGCGCAAGAAGCGGTGCTCTTCTGCGCTG 120
 Db 21 ArgLysSerSerThrProGluGluValLysLysLysLysLysLysLysLysLysLys 40
 QY 121 AGTGAGGCAAGAAGCAACATCATCTCTGGAGAGGGGCAAGAGAGATCTGTGGCGGATGTG 180
 Db 41 SerGluAspLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 60
 QY 181 GGCCAGACTGTCAGCAGTCCCTACGCCACCTTTGTCAAGATGCTGCCAGATAAGGACTGC 240
 Db 61 GlyGlnThrValAspAspProTyrAlaThrPheValLysMetLeuProAspLysAspCys 80
 QY 241 CGTATGCTCTTATGATGCACTATGAGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
 Db 81 ArgTyrAlaLeuTyrAspAlaThrTyrGluThrLysSerLysLysGluAspLeuVal 100
 QY 301 TTTATCTTCTGGCCCGCCAGTCTGCCCTTAAAGAGCAAAATGATTTATGCGACTCC 360
 Db 101 PheIlePheTrpAlaProGluSerAlaProLeuLysSerLysMetIleTyrAlaSerSer 120
 QY 361 AAGGAGCCCATCAAGAGAGCTCAGGAGATCAAGGATCAAGTGAATGCAAGCAAACTGCTAC 420
 Db 121 LysAspAlaIleLysLysLysLysLeuThrGlyIleHisGluLeuGlnAlaAsnCysTyr 140
 QY 421 GAGGAGTCAAGACCGCTGACCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
 Db 141 GluGluValLysAspArgCysThrLeuAlaGluLysLeuGlyGlySerAlaValIleSer 160
 QY 481 CTGGAGGCAAGCCTTTG 498
 Db 161 LeuGluGlyLysProLeu 166
 RESULT 4
 AD005889
 ID AD005889 standard; protein; 166 AA.
 AC AD005889;
 XX
 DT 15-JUL-2004 (first entry)
 XX
 DE Human cofillin polypeptide.
 XX
 KW Cofilin; inflammatory disease; antiasthmatic; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2004035092-A2.
 XX

PD 29-APR-2004.
XX
PF 15-OCT-2003; 2003WO-GB004450.
XX
PR 15-OCT-2002; 2002GB-00024014.
XX
XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
PA (FARB) BAYER HEALTHCARE AG.
XX
XX Bacon KB, Herath HMA, Liu N, Rohlff C;
XX WPI; 2004-348336/32.
DR N-PSDB; ADO05890.
XX
XX Treating or preventing an inflammatory disease, e.g., asthma comprises
PT administering to a subject an agonist or antagonist of cofilin isoform 1
PT or 2 that modulates the expression or activity of a cofilin polypeptide.
XX
XX Claim 6; SEQ ID NO 1; 47pp; English.
XX
CC The invention relates to treating or preventing an inflammatory disease
CC and involves administering to a subject, an agent that modulates the
CC expression or activity of a cofilin polypeptide. The agent is an agonist
CC or antagonist of cofilin isoform 1 or 2. Antiasthmatic. The method is
CC useful in treating or preventing an inflammatory disease, e.g., asthma.
CC The present sequence represents a human cofilin polypeptide.
XX
SQ Sequence 166 AA;

Alignment Scores:
Pred. No.: 1.43e-82 Length: 166
Score: 846.00 Matches: 166
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 93.90% Indels: 0
DB: 8 Gaps: 0

US-10-649-952A-2 (1-501) x ADO05889 (1-166)
Qy 1 ATGCCCTCCGGTGGCTGCTCTGATGCTCATCAAGGTGTTCAACGACATGAAGTG 60
Db 1 MetAlaSerGlyValAlaValSerAspGlyValIleLysValPheAsnAspMetLysVal 20
Qy 61 CGTAAGTCTTCAACGCCAGAGGAGGTGAGAGGCGCAAGAGCGGTCTCTCTGCTG 120
Db 21 ArgLysSerThrProGluGluValLysLysArgLysLysAlaValLeuPheCysLeu 40
Qy 121 AGTGAGGACAGAAAGAACATCATCTGGAGGAGGCGCAAGAGATCCCTGGTGGCGATGTG 180
Db 41 SerGluAspLysLysAsnIleLeuGluGluGlyLysGluIleLeuValGlyAspVal 60
Qy 181 GGCAGAGTCTGACAGATCCCTACGCCACCTTTCTCAAGATGCTGCCAGATAAGATGTC 240
Db 61 GlyGlnThrValAspAspProTyrAlaThrPheValLysMetLeuProAspLysAspCys 80
Qy 241 CGCTATGCCCTCTATGATGCAACCTATGACACCAAGGAGGAGGAGGAGGATCTGCTG 300
Db 81 ArgTyrAlaLeuTyrAspAlaThrTyrGluThrLysGluSerLysLysGluAspLeuVal 100
Qy 301 TTTATCTTCTGGGCCCGGAGTCTGCGCCCTTAAGAGCAAAATGATTATGCCAGCTCC 360
Db 101 PheIlePheThrAlaProGluSerAlaProLeuLysSerLysMetIleTyrAlaSerSer 120
Qy 361 AAGACGCCATCAAGAGAAGCTGACAGGATCAAGCATGATTAATGCAAGCAAACTGTAC 420
Db 121 LysAspAlaIleLysLysLeuThrGlyIleLysHisGluLeuGlnAlaAsnCysTyr 140
Qy 421 GAGGAGTCAAGGACCGCTGCACCTGGCAGAGAGTGGGGGCGAGTGGGTCATCTCC 480
Db 141 GluGluValLysAspArgCysThrLeuAlaGluLysLeuGlyGlySerAlaValIleSer 160
Qy 481 CTGGAGGCGCAAGCCTTTG 498

Db 161 LeuGluGlyLysProLeu 166
RESULT.5
ADQ30534
ID ADQ30534 standard; protein; 166 AA.
XX
XX AC ADQ30534;
XX
DT 23-SEP-2004 (first entry)
XX
XX Pancreas cancer marker - non-muscle cofilin isoform.
XX cytostatic; diagnosis; pancreatic cancer; antibody; antisense construct;
XX differential expression.
XX
XX Homo sapiens.
XX
XX WO2004055519-A2.
XX
XX 01-JUL-2004.
XX
XX 11-DEC-2003; 2003WO-EP014057.
XX
XX 17-DEC-2002; 2002EP-00028058.
PR 05-NOV-2003; 2003EP-00025237.
XX
XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
PA (SINO-) SINOGENOMAX CO LTD CHINESE NAT HUMAN GEN.
XX
XX Chen J, Hu L, Liu TH, Lu ZH, Shen Y;
PI WPI; 2004-488121/46.
DR
XX
XX New specific markers comprises at least one polypeptide up-regulated in
PT pancreatic cancer, useful for diagnosing pancreatic cancer.
PT
XX
XX Claim 1; SEQ ID NO 21; 381pp; English.
XX
CC The invention relates to a marker (I) for diagnosis of pancreatic cancer
CC comprising at least one polypeptide selected from 55 proteins up-
CC regulated in pancreatic cancer (Table 2 and Table 3, given in the
CC specification) or from 68 proteins with higher levels in pancreatic
CC cancer compared to normal tissue (Table 6, given in the specification).
CC (I) is a polypeptide for use as a marker or as a component of a marker
CC for diagnosis of pancreatic cancer and/or the susceptibility to
CC pancreatic cancer. A compound (antibody, an antibody-derivative, an
CC antibody fragment, a peptide, or an antisense construct) identified by
CC screening methods using (I) is useful for treatment or prevention of
CC pancreatic cancer. It is also useful for the preparation of a diagnostic
CC composition for diagnosing pancreatic cancer or a predisposition for
CC pancreatic cancer. The current polypeptides were found to be
CC differentially expressed in pancreatic tissue obtained from individuals
CC suffering from pancreatic cancer as compared to healthy pancreatic
CC tissue. They have been identified as suitable as markers of pancreatic
CC cancer for early diagnosis of the disease. This sequence corresponds to a
CC protein marker of the invention.
XX
SQ Sequence 166 AA;

Alignment Scores:
Pred. No.: 1.43e-82 Length: 166
Score: 846.00 Matches: 166
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 93.90% Indels: 0
DB: 8 Gaps: 0

US-10-649-952A-2 (1-501) x ADQ30534 (1-166)
Qy 1 ATGCCCTCCGGTGGCTGCTCTGATGCTCATCAAGGTGTTCAACGACATGAAGTG 60
Db 1 MetAlaSerGlyValAlaValSerAspGlyValIleLysValPheAsnAspMetLysVal 20

QY 61 CGTAAGTCTTCAAGCCAGAGGAGGTGAGAGCGCAAGAGCGGTGCTCTTCTGCGCTG 120
 Db 21 ArgLysSerSerThrProGluGluValLysLysArgLysLysAlaValLeuPheCysLeu 40
 QY 121 AGTGAGGACAAAGAACATCATCTCGAGGAGGCAAGAGATCTCTGGTGGCGATGTG 180
 Db 41 SerGluAspLysLysAsnIleLeuGluGluGlyLysGluIleLeuValGlyAspVal 60
 QY 181 GGCAGAGCTCGACGATCCCTACGCCACCTTTGTCAAGATGCTGCAGATAAGGACTGC 240
 Db 61 GlyGlnThrValAspAspProTyrAlaThrPheValLysMetLeuProAspLysAspCys 80
 QY 241 CGCTATGCGCTCTATGATGCAACTATGAGACCAAGAGAGCAAGAGGATCTGGTG 300
 Db 81 ArgTyrAlaLeuTyrAspAlaThrTyrGluThrLysGluSerLysLysGluAspLeuVal 100
 QY 301 TTTATCTTCTGGGCCCCGAGTCTGGCCCTTAAGAGCAAAATGATTATGACGCTCC 360
 Db 101 PheIlePheTrpAlaProGluSerAlaProLeuLysSerLysMetIleTyrAlaSerSer 120
 QY 361 AAGGAGCCCATCAAGAGAGCTGACAGGAGTCAAGCATGAATTGCAAGCAAACTGCTAC 420
 Db 121 LysAspAlaIleLysLysLysLeuThrGlyIleLysHisGluLeuGlnAlaAsnCysTyr 140
 QY 421 GAGGAGTCAAGGACCGCTGCACCTGCGAGAGAGCTGGGGGCGAGTGGGTCATCTCC 480
 Db 141 GluGluValLysAspArgCysThrLeuAlaGluLysLeuGlyGlySerAlaValIleSer 160
 QY 481 CTGGAGGGCAAGCCTTTG 498
 Db 161 LeuGluGlyLysProLeu 166

RESULT 6
 ADQ65133
 ID ADQ65133 standard; protein; 229 AA.
 XX AC ADQ65133;
 XX DT 07-OCT-2004 (first entry)
 XX DE Novel human protein sequence #106.
 XX KW osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;
 KW gene therapy; diagnostic marker; morbid state; osteoporosis;
 KW neurological disease; Alzheimer's disease; Parkinson's disease; dementia;
 KW cancer.
 XX OS Homo sapiens.
 XX PN EP1440981-A2.
 XX PD 28-JUL-2004.
 XX PF 21-JAN-2004; 2004BP-00001196.
 XX PR 21-JAN-2003; 2003JP-00102206.
 XX PR 09-MAY-2003; 2003JP-00131392.
 XX PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 XX PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
 PI Yamamoto J, Isono Y, Nagai K, Irie R;
 XX DR WPI: 2004-535376/52.
 XX DR N-PSDB; ADQ62945.
 XX PT Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases,
 PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
 XX PS Claim 1; SEQ ID NO 2294; 2449pp; English.
 XX CC The invention relates to 2495 novel polynucleotides (1) and their encoded
 CC polypeptides, sequences hybridizing to these nucleotides, sequences

CC encoding partial polypeptides and sequences having 70% or 90% identity to
 CC the nucleotide and protein sequences. The nucleotides and polypeptides
 CC are useful as diagnostic markers or therapeutic target for the diseases
 CC or morbid states. They are also useful for treating osteoporosis,
 CC neurological diseases, Alzheimer's diseases, Parkinson's diseases,
 CC dementia and various cancers. This sequence corresponds to a protein
 CC sequence of the invention.
 XX SQ Sequence 229 AA;

Alignment Scores:
 Pred. No.: 1.58e-82 Length: 229
 Score: 846.00 Matches: 166
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 93.90% Indels: 0
 DB: 8 Gaps: 0

US-10-649-952A-2 (1-501) x ADQ65133 (1-229)

QY 1 ATGGCTCTCGGTGCTGCTGCTGATGCTCATCAAGTGTTCACGACATGAAGTGTG 60
 Db 64 MetAlaSerGlyValAlaValSerAspGlyValIleLysValPheAsnAspMetLysVal 83
 QY 61 CGTAAGTCTTCAAGCGCAGAGGAGGTGAAGAGCGCAAGAGCGGTGCTCTTCTGCGCTG 120
 Db 84 ArgLysSerSerThrProGluGluValLysLysArgLysLysAlaValLeuPheCysLeu 103
 QY 121 AGTGAGGACAAAGAAACATCATCTCTGGAGGAGGCAAGAGATCTCTGGTGGCGATGTG 180
 Db 104 SerGluAspLysLysAsnIleLeuGluGluGlyLysGluIleLeuValGlyAspVal 123
 QY 181 GGCGAGCTGTGACGATCCCTACGCGCTTGTCAAGATGCTGCAGATAAGGACTGC 240
 Db 124 GlyGlnThrValAspAspProTyrAlaThrPheValLysMetLeuProAspLysAspCys 143
 QY 241 CGCTATGCGCTCTATGATGCAACCTATGAGACCAAGGAGAGCAAGAGGAGTCTGGTG 300
 Db 144 ArgTyrAlaLeuTyrAspAlaThrTyrGluThrLysGluSerLysLysGluAspLeuVal 163
 QY 301 TTTATCTTCTGGGCCCCGAGTCTGGCCCTTAAGAGCAAAATGATTATGACGCTCC 360
 Db 164 PheIlePheTrpAlaProGluSerAlaProLeuLysSerLysMetIleTyrAlaSerSer 183
 QY 361 AAGGAGCCCATCAAGAGAGCTGACAGGAGTCAAGCATGAATTGCAAGCAAACTGCTAC 420
 Db 184 LysAspAlaIleLysLysLysLeuThrGlyIleLysHisGluLeuGlnAlaAsnCysTyr 203
 QY 421 GAGGAGGTCAAGGACCGCTGCACCTGCGAGAGAGTGGGGGCGAGTGGGTCATCTCC 480
 Db 204 GluGluValLysAspArgCysThrLeuAlaGluLysLeuGlyGlySerAlaValIleSer 223
 QY 481 CTGGAGGGCAAGCCTTTG 498
 Db 224 LeuGluGlyLysProLeu 229

RESULT 7
 ABR41637
 ID ABR41637 standard; protein; 187 AA.
 XX AC ABR41637;
 XX DT 02-JUN-2003 (first entry)
 XX DE Human DITHP cytoskeletal protein.
 XX KW Human; dithp; diagnostic and therapeutic polynucleotide; diagnosis;
 KW cancer; cell proliferative disorder; autoimmune disorder;
 KW inflammatory disorder; infection; hormonal disorder; metabolic disorder;
 KW neurological disorder; gastrointestinal disorder; transport disorder;
 KW connective tissue disorder; drug screening; proteome analysis;
 KW gene therapy; antisense therapy; genotyping; transgenic animal; knock in;
 KW disease model; toxicological testing; transcript imaging;

KW cytoskeletal protein.

OS Homo sapiens.

XX WO200297031-A2.

XX 05-DEC-2002.

XX 27-MAR-2002; 2002WO-US010056.

XX 28-MAR-2001; 2001US-0279619P.

XX 29-MAR-2001; 2001US-0280067P.

XX 29-MAR-2001; 2001US-0280068P.

XX 16-MAY-2001; 2001US-0291280P.

XX 17-MAY-2001; 2001US-0291829P.

XX 17-MAY-2001; 2001US-0291849P.

XX 19-JUN-2001; 2001US-0299428P.

XX 20-JUN-2001; 2001US-0299776P.

XX 20-JUN-2001; 2001US-0300001P.

XX (INCYTE GENOMICS INC.

XX Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;

XX Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshay SR;

XX Daugherty SC, Dam TC, Liu TP, Nguyen DA, Kleefeld Y, Gerstin EH;

XX Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;

XX Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;

XX WPI; 2003-129518/12.

XX N-PSDB; ACC46574.

XX Novel human diagnostic and therapeutic polypeptide useful for identifying

XX test compound which specifically binds to a polypeptide encoded by human

XX diagnostic and therapeutic polynucleotide, and to induce antibodies.

XX Claim 27; SEQ ID NO 1172; 591pp; English.

XX The invention relates to novel human diagnostic and therapeutic
 XX polynucleotides designated dithp (ACC46080-ACC46749) and to their encoded
 XX proteins (DITHP; ABR41136-ABR41812). The invention also relates to
 XX polynucleotide sequences at least 90% identical to the dithp cDNA
 XX sequences of the invention; recombinant vectors, host cells and
 XX transgenic organisms comprising a dithp nucleic acid sequence; the
 XX recombinant production of DITHP proteins; antibodies specific for DITHP
 XX proteins; microarrays comprising dithp nucleic acid sequences; methods of
 XX detecting dithp nucleotide and protein sequences; methods of screening
 XX for compounds which specifically bind a DITHP protein; and methods of
 XX assessing the toxicity of test compounds using a dithp hybridisation
 XX probe. Dithp nucleic acid sequences and DITHP proteins may be used in the
 XX diagnosis of a wide variety of conditions including cancer and other cell
 XX proliferative disorders; autoimmune or inflammatory disorders; bacterial,
 XX viral, fungal or parasitic infections; hormonal disorders; metabolic
 XX disorders; neurological disorders; gastrointestinal disorders; transport
 XX disorders; and connective tissue disorders. They may also be used to
 XX screen for modulators of protein activity or gene expression. DITHP
 XX proteins can additionally be used in analysis of the proteome of a tissue
 XX or cell type and to induce antibodies. The dithp nucleic acids are
 XX additionally useful in somatic or germline gene therapy of the disorders
 XX mentioned above, as a source of antisense sequences, as a source of
 XX probes and primers, in genotyping and identification of individuals, in
 XX the generation of transgenic animal models of human disease or knock in
 XX humanised animals, in toxicological testing, and in transcript imaging.
 XX The present sequence represents a DITHP protein which is a cytoskeletal
 XX protein. Note: the sequence data for this patent did not form part of the
 XX printed specification, but was obtained in electronic format directly
 XX from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 187 AA;

XX Alignment Scores:

XX Pred. No.: 4.03e-82 Length: 187

XX Score: 842.00 Matches: 165

XX Percent Similarity: 99.40% Conservative: 0

Best Local Similarity:	99.40%	Mismatches:	1
Query Match:	93.45%	Indels:	0
DB:	6	Gaps:	0
US-10-649-952A-2 (1-501) x ABR41637 (1-187)			
Qy	1	ATGGCCTCCGGTGTGGCTGTCTCTGATGGTGTTCATCAAGGTGTTCAACGACATCAAGGTG	60
Db	22	MetAlaSerGlyValAlaValSerAspGlyValIleLysValPheAsnAspMetLysVal	41
Qy	61	CGTAAGTCTTCAACGCCAGAGAGAGGTGCAAGAGCGCAAGAGCGGCTCTTCTGCTG	120
Db	42	ArgLysSerSerThrProGluGluValLysArgLysLysAlaValLeuPheCysLeu	61
Qy	121	AGTGAGGACAAGAAGAACATCATCCTCGAGGAGGCAAGAGAGATCCTGGTGGGCGCATGTG	180
Db	62	SerGluAspLysLysAsnIleIleLeuGluGluGlyLysGluLeuValGlyAspVal	81
Qy	181	GGCCAGACTGTGACGATCCCTACGCCACCTTTGTCAAGATGCTGCCAGATAAGGACTGC	240
Db	82	GlyGlnThrValAspAspProTyrThrThrPheValLysMetLeuProAspLysAspCys	101
Qy	241	CGCTATGCCCTCTATGATGCAACCTATGACACCAAGAGAGCAAGAGAGGATCTGGTG	300
Db	102	ArgTyrAlaLeuTyrAspAlaThrTyrGluThrLysGluSerLysLysGluAspLeuVal	121
Qy	301	TTTATCTTCGGGCCCCCGAGTCTGGCCCTTTAAGAGCAAAATGATTATGCCAGCTCC	360
Db	122	PheIlePheIlePalaProGluSerAlaProLeuLysSerLysMetIleTyrAlaSerSer	141
Qy	361	AAGGACGCCCTCAAGAGAAAGCTGACAGGATCAAGCATGAATTGCAAGCAAACTGCTAC	420
Db	142	LysAspAlaIleLysLysLysLeuThrGlyIleLysHisGluLeuGlnAlaAsnCysTyr	161
Qy	421	GAGAGGTCAAGGACCCCTGACCCCTGGCAGAGAGCTGGGGGGCAGTGGCGTCACTCC	480
Db	162	GluGluValLysAspArgCysThrLeuAlaGluLysLeuGlyGlySerAlaValIleSer	181
Qy	481	CTGGAGGGCAAGCCTTTG 498	
Db	182	LeuGluGlyLysProLeu 187	
RESULT 8			
ADN99790	ADN99790 standard; protein; 239 AA.		
ID	ADN99790		
XX	AC ADN99790;		
XX	29-JUL-2004 (first entry)		
XX	Novel human protein sequence #606.		
XX	anti-inflammatory; dermatological; neuroprotective; immunomodulator;		
XX	antibacterial; virucide; antipsoriatic; cytostatic; gene therapy;		
XX	vaccine; inflammatory; CNS; immune disorder; cancer; psoriasis; diabetes;		
XX	early aging; hormonal imbalance; ischemic heart disease;		
XX	ulcerative colitis.		
OS	Homo sapiens.		
XX	WO2004038003-A2.		
XX	06-MAY-2004.		
XX	24-OCT-2003; 2003WO-US033947.		
XX	25-OCT-2002; 2002US-0421061P.		
XX	25-OCT-2002; 2002US-0421080P.		
XX	25-OCT-2002; 2002US-0421552P.		
XX	25-OCT-2002; 2002US-0421614P.		
XX	30-OCT-2002; 2002US-0422177P.		
XX	30-OCT-2002; 2002US-0422178P.		
XX	15-NOV-2002; 2002US-0426355P.		

PR 15-NOV-2002; 2002US-0426384P.
 PR 15-NOV-2002; 2002US-0426394P.
 PR 15-NOV-2002; 2002US-0426430P.
 PR 15-NOV-2002; 2002US-0426916P.
 PR 27-NOV-2002; 2002US-0429224P.
 PR 27-NOV-2002; 2002US-0429275P.
 PR 27-NOV-2002; 2002US-0429302P.
 PR 27-NOV-2002; 2002US-0429326P.
 PR 27-NOV-2002; 2002US-0429651P.
 PR 04-DEC-2002; 2002US-0430645P.
 PR 04-DEC-2002; 2002US-0430651P.
 PR 04-DEC-2002; 2002US-0430657P.
 PR 04-DEC-2002; 2002US-0430663P.
 PR 04-DEC-2002; 2002US-0430688P.
 PR 04-DEC-2002; 2002US-0430684P.
 PR 05-DEC-2002; 2002US-0430937P.
 PR 05-DEC-2002; 2002US-0430965P.
 PR 12-DEC-2002; 2002US-0431458P.
 PR 12-DEC-2002; 2002US-0433251P.
 PR 12-DEC-2002; 2002US-0433500P.
 PR 13-DEC-2002; 2002US-0433316P.
 PR 13-DEC-2002; 2002US-0433318P.
 PR 23-DEC-2002; 2002US-0436236P.
 PR 03-JAN-2003; 2003US-0437914P.
 PR 17-JAN-2003; 2003US-0440820P.
 PR 17-JAN-2003; 2003US-0440821P.
 PR 18-APR-2003; 2003US-0463700P.
 PR 18-APR-2003; 2003US-0463708P.
 PR 18-APR-2003; 2003US-0463716P.
 PR 18-APR-2003; 2003US-0463732P.
 PR 02-MAY-2003; 2003US-0467199P.
 PR 02-MAY-2003; 2003US-0467201P.
 PR 02-MAY-2003; 2003US-0467203P.
 PR 02-MAY-2003; 2003US-0467230P.
 PR 15-MAY-2003; 2003US-0471306P.
 PR 15-MAY-2003; 2003US-0471336P.
 PR 22-MAY-2003; 2003US-0472420P.
 PR 22-MAY-2003; 2003US-0472430P.
 PR 09-JUN-2003; 2003US-0476609P.
 PR 09-JUN-2003; 2003US-0476621P.
 PR 09-JUN-2003; 2003US-0476632P.
 PR 09-JUN-2003; 2003US-0476641P.
 PR 08-JUL-2003; 2003US-0485217P.
 PR 08-JUL-2003; 2003US-0485218P.
 PR 08-JUL-2003; 2003US-0485223P.
 PR 08-JUL-2003; 2003US-0485224P.
 PR 08-JUL-2003; 2003US-0485325P.
 PR 08-JUL-2003; 2003US-0485359P.
 PR 14-JUL-2003; 2003US-0486446P.
 PR 14-JUL-2003; 2003US-0486480P.
 PR 15-JUL-2003; 2003US-0486891P.
 PR 15-JUL-2003; 2003US-0486960P.
 PR 08-AUG-2003; 2003US-0493341P.
 PR 08-AUG-2003; 2003US-0493341P.
 PR 08-AUG-2003; 2003US-0493370P.
 PR 08-AUG-2003; 2003US-0493573P.
 PR 08-AUG-2003; 2003US-0493577P.
 XX
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
 XX
 PI Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;
 PI Halenbeck RF, Kothakota S, Lin H, Linnemann T, Pierce K, Wang Y;
 PI Wong JGP, Wu G, Zhang H, Zeng C;
 XX
 DR WPI; 2004-365511/34.
 DR N:PSDB; ADN99006.
 XX
 PT New nucleic acid molecules, useful in preparing a composition for
 PT treating or preventing e.g. inflammatory, CNS, bacterial or viral
 PT disorders, cancer, psoriasis, diabetes, ischemic heart disease or
 PT ulcerative colitis.
 XX
 PS Claim 14; SEQ ID NO 1390; 532pp; English.

CC The invention relates to a nucleic acid molecule comprising a
 CC polynucleotide sequence or its complement that encodes a polypeptide. The
 CC nucleic acid is useful in preparing a composition for treating or
 CC preventing inflammatory, CNS, immune, bacterial or viral disorder,
 CC cancer, psoriasis, diabetes, early aging, hormonal imbalance, ischemic
 CC heart disease or ulcerative colitis. This sequence corresponds to a
 CC protein of the invention.
 XX
 SQ Sequence 239 AA;
 Alignment Scores:
 Pred. No.: 5,6e-82 Length: 239
 Score: 841.00 Matches: 165
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 93.34% Indels: 0
 DB: 8 Gaps: 0
 US-10-649-952A-2 (1-501) x ADN99790 (1-239)
 QY 4 GCCTCCGGTGTGGCTCTCTCTGATGTGTTCATCAAGGTGTTCACGACATGAAGTGCCT 63
 Db 75 AlaSerGlyValAlaValSerAspGlyValIleLysValPheAsnAspMetLysValArg 94
 QY 64 AGTCTTCAACGCCAGAGGAGGTGAAGAGCGCAAGCGGTGCTCTTCTCCCTGAGT 123
 Db 95 LysSerSerThrProGluGluValLysLysArgLysLysAlaValLeuPheCysLeuSer 114
 QY 124 GAGGACAAGAACATCATCTCTGGAGGAGGCGCAGGATCTGCTGGCGATGTGGGC 183
 Db 115 GluAspLysLysAsnIleIleLeuGluGluGlyLysGluIleLeuValGlyAspValGly 134
 QY 184 CAGACTGTGCGAGGATCCCTACGCCACTTTGTCAAGATGCTGCAGATAAGGACTGCCGC 243
 Db 135 GlnThrValAspAspProTyrAlaThrPheValLysMetLeuProAspLysAspCysArg 154
 QY 244 TATGCCCTCTATGATGCAACCTATGAGACCAAGGAGGAGCAAGAGGAGGATCTGGTGT 303
 Db 155 TyrAlaLeuTyrAspAlaThrTyrGluThrLysGluSerLysLysGluAspLeuValPhe 174
 QY 304 ATCTTCTGGGCCCCGAGTCTGGCCCCCTTAGAGCAAAATGATTTATGCCAGCTCAAG 363
 Db 175 IlePheTrpAlaProGluSerAlaProLeuLysSerLysMetIleTyrAlaSerSerLys 194
 QY 364 GACGCCATCAAGAAGAGCTGACAGGATCAAGCATGAATTCAGCAAACTCTACGAG 423
 Db 195 AspAlaIleLysLysLysLeuThrGlyIleLysHisGluLeuGlnAlaAsnCysTyrGlu 214
 QY 424 GAGGTCAAGGACCGCTGCACCTGCGAGAGAGCTGGGGGCGAGTCCGGTCAATCTCCCTG 483
 Db 215 GluValLysAspArgCysThrLeuAlaGluLysLeuGlyGlySerAlaValIleSerLeu 234
 QY 484 GAGGGCAGCCTTTG 498
 Db 235 GluGlyLysProLeu 239
 RESULT 9
 ADJ70464
 ID ADJ70464 standard; protein; 149 AA.
 XX
 AC ADJ70464;
 XX
 DT
 XX 06-MAY-2004 (first entry)
 DE Human heat mitochondrial protein as a therapeutic target SeqID2270.
 XX
 KW mitochondrial; human; screening assay; diabetes mellitus;
 KW Huntington's disease; osteoarthritis;
 KW Leber's hereditary optic neuropathy; LHON;
 KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
 KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
 KW neuroprotective; neurotropic; antidiabetic; anticonvulsant; antiarthritic;
 KW osteopathic; ophthalmological; cytostatic.

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XX OS Homo sapiens.
XX PN WO2003087768-A2.
XX XX 23-OCT-2003.
XX XX 04-APR-2003; 2003WO-US010870.
XX XX 12-APR-2002; 2002US-0372843P.
XX PR 17-JUN-2002; 2002US-0389987P.
XX PR 20-SEP-2002; 2002US-0412418P.
XX XX (MITO-) MITOKOR.
XX PA (BUCK-) BUCK INST AGE RES.
XX XX Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GW;
XX FI Warnock DE;
XX XX WPI; 2003-845369/78.
XX XX Identifying a mitochondrial target for drug screening assays and for
XX PT treating diseases associated with altered mitochondrial function,
XX PT comprises detecting a modified polypeptide in a sample and correlating
XX PT with the disease.
XX XX Claim 1; SEQ ID NO 2270; 180pp; English.
XX XX This invention relates to novel mitochondrial targets that can be used
XX CC for therapeutic intervention in treating a disease associated with
XX CC altered mitochondrial function. Specifically, it refers to a method for
XX CC identifying proteins of the human heart mitochondrial proteome that are
XX CC useful for drug screening assays, as well as therapeutic targets. The
XX CC present invention describes a method for identifying such proteins that
XX CC can be used in the treatment of various diseases associated with altered
XX CC mitochondrial function including diabetes mellitus, Huntington's disease,
XX CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
XX CC ecephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
XX CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
XX CC compositions have neuroprotective, neurotropic, antidiabetic,
XX CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
XX CC cytoskeletal activities. This polypeptide sequence is a human heart
XX CC mitochondrial protein of the invention.
XX XX Sequence 149 AA;

Alignment Scores:
Pred. No.: 1.07e-73 Length: 149
Score: 764.00 Matches: 149
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 84.79% Indels: 0
DB: 7 Gaps: 0

US-10-649-952A-2 (1-501) x ADJ70464 (1-149)
QY 52 ATGAGGTGCTAGTCTTCAACCCAGAGAGGTGAAGCCCAAGAGCCGAGCGGTGCTC 111
DB 1 MetLysValArgLysSerThrProGluValLysArgLysLysAlaValLeu 20
QY 112 TTCTGCTGAGTGGAGCAAGAACATCATCTCGGAGGAGGCAAGGAGATCCTGTG 171
DB 21 PheCysLeuSerGluAspLysLysAsnIleLeuGluGluLysGluIleLeuVal 40
QY 172 GGCATGTGGCCAGACTGTGCAGCATCCCTACGCCACCTTTGTCAAGATGCTCCAGAT 231
DB 41 GlyAspValGlyGlnThrValAspAspProTyrAlaThrPheValLysMetLeuProAsp 60
QY 232 AAGACTGCCCTATGCCCTTATGATCCACCTATGACCAAGGAGGCAAGAGGAG 291
DB 61 LysAspCysArgTyrAlaLeuTyrAspAlaThrTyrGluThrLysGluSerLysGlu 80
QY 292 GATCTGGTGTATTATCTTCTGGGCCCCCGAGTCTGCGCCCTTAAGAGCAAAATGATTAT 351

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DB 81 AspLeuValPheIlePheTyrAlaProGluSerAlaProLeuLysSerLysMetIleTyr 100
QY 352 GCAGACTCCCAAGGACGCCATCAAGAGAAGCTGACAGGGATCAAGCATGATTCACAGCA 411
DB 101 AlaSerSerLysAspAlaIleLysLysLysLeuThrGlyLysHisGluLeuGlnAla 120
QY 412 AACTGTACGAGGAGGTCAAGGACCGCTGCACCTGCGCAGAGAAGCTGGGGGCGAGTGGC 471
DB 121 AsnCysTyrGluGluValLysAspArgCysThrLeuAlaGluLysLeuGlyGlySerAla 140
QY 472 GTCATCTCCCTGGAGGCAAGCCCTTTG 498
DB 141 ValIleSerLeuGluGlyLysProLeu 149

RESULT 10
ABR41956
ID ABR41956 standard; protein; 166 AA.
XX AC ABR41956;
XX DT 11-AUG-2003 (first entry)
XX DE Mouse cofilin, implicated in pain.
XX KW Mouse; cofilin; nociceptive; analgesic; signal transduction;
XX OS Mus musculus.
XX PN EPI281775-A2.
XX PD 05-FEB-2003.
XX PF 26-JUL-2002; 2002EP-00255231.
XX PR 27-JUL-2001; 2001GB-00018354.
XX PR 07-FEB-2002; 2002GB-00002892.
XX PA (WARN ) WARNER LAMBERT CO.
XX PI Brooksbank RA, Dixon AK, Lee K, Pinnock RD;
XX WPI; 2003-335005/32.
XX N-PSDB; ACC48821.
XX PT Use of isolated gene or nucleic acid sequence, recombinant vector, host
XX PT cell, non-human animal, polypeptide encoded by the nucleic acid sequence,
XX PT or antibody, for screening of compounds for the treatment of pain, or for
XX PT diagnosing pain.
XX PS Disclosure; Page 65-66; 87pp; English.
XX CC The present sequence is the protein sequence of mouse cofilin. This is
XX CC encoded by a gene that has been identified as being up-regulated in 2
XX CC models of chronic pain, i.e. streptozocin-induced diabetes and chronic
XX CC constrictive injury to a nerve leading to the spine. The expression
XX CC products of such genes can be used to screen libraries for compounds and
XX CC peptide agonists and antagonists of gene product activity that may be
XX CC useful in the treatment or prevention of chronic pain, and in the
XX CC development of diagnostic tools for the identification and
XX CC characterisation of pain
XX SQ Sequence 166 AA;

Alignment Scores:
Pred. No.: 5.88e-67 Length: 166
Score: 702.00 Matches: 135
Percent Similarity: 89.76% Conservative: 14
Best Local Similarity: 81.33% Mismatches: 17
Query Match: 77.91% Indels: 0
DB: 6 Gaps: 0

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US-10-649-952A-2 (1-501) x ABR41956 (1-166)
QY 1 ATGGCCCTCGGTGGCTGCTCTGATGCTGATCAAGGTGTTCAACGACATGAAGGTG 60
Db 1 MetAlaSerGlyValThrValAsnAspGluValIleLysValPheAsnAspMetLysVal 20
QY 61 CGTAAGTCTTCAACGCCAGAGGAGGTGAAGAGCGCAAGAGCGGTGCTCTTCGCTG 120
Db 21 ArgLysSerSerThrGlnGluGluIleLysLysArgLysLysAlaValLeuPheCysLeu 40
QY 121 AGTGAGGACCAAGAACATCATCTCGAGGAGGCAAGAGATCCTGTTGGGCGATGTG 180
Db 41 SerAspAspLysArgGlnIleValGluAlaLysGlnIleLysGlnIleValGlyAspIle 60
QY 181 GGCAGAGCTGTCAGCATCCTACGCCACCTTTGTCAGATGTCGCAGATAAGGACTGC 240
Db 61 GlyAspThrValGluAspProTyrThrSerPheValLysLeuLeuProLeuAsnAspCys 80
QY 241 CGCTATGCCCTCTATGATCAACCTATGAGACCAAGAGGAGGAGGAGGAGGATCTGGT 300
Db 81 ArgTyrAlaLeuTyrAspAlaThrTyrGluThrLysGluSerLysLysGluAspLeuVal 100
QY 301 TTTATCTTCTGGGCCCCCGAGTCTGCGCCCTTAAGAGCAAAATGATTATGCCAGTCC 360
Db 101 PheIlePheTrpAlaProGluSerAlaProLeuLysSerLysMetIleTyrAlaSerSer 120
QY 361 AAGGAGCGCCATCAAGAAAGAGTGCAGGAGTCAAGCATGAATTGCAAGCAAACTGCTAC 420
Db 121 LysAspAlaIleLysLysLysPheThrGlyIleLysHisGluTrpGlnValAsnGlyLeu 140
QY 421 GAGGAGGTCAAGGACCGCTGCACCTCGCAGAGAGAGTGGGGGCGAGTGGCGTCACTCC 480
Db 141 AspAspIleLysAspArgSerThrLeuGlyGluLysLeuGlySerValValSer 160
QY 481 CTGAGGGCAAGCCTTTG 498
Db 161 LeuGluGlyLysProLeu 166

RESULT 11
ID AAM78545
AA AAM78545 standard; protein; 166 AA.
AC AAM78545;
XX
XX
DT 06-NOV-2001 (first entry)
DE Human protein SEQ ID NO 1207.
XX
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation.
XX
OS Homo sapiens.
XX
XX WO200157190-A2.
XX
XX 09-AUG-2001.
XX
XX 05-FEB-2001; 2001WO-US004098.
XX
XX 03-FEB-2000; 2000US-00496914.
XX
XX 27-APR-2000; 2000US-00560875.
XX
XX 20-JUN-2000; 2000US-00598075.
XX
XX 19-JUL-2000; 2000US-00620325.
XX
XX 01-SEP-2000; 2000US-00654936.
XX
XX 15-SEP-2000; 2000US-00663561.
XX
XX 20-OCT-2000; 2000US-00693325.
XX
XX 30-NOV-2000; 2000US-00728422.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
PI

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PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AU, Yang Y, Wejhrman T, Goodrich R;
XX
DR WPI; 2001-476283/51.
DR N-PSDB; AAK51678.
XX
XX Nucleic acids encoding polypeptides with cytokine-like activities, useful
PT in diagnosis and gene therapy.
XX
XX Claim 20; Page 3461-3462; 6221pp; English.
XX
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity relating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
CC sequence listing were missing at the time of publication
XX
SQ Sequence 166 AA;

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Alignment Scores:
Pred. No.: 1 246-66 Length: 166
Score: 699.00 Matches: 134
Percent Similarity: 89.76% Conservative: 15
Best Local Similarity: 80.72% Mismatches: 17
Query Match: 77.58% Indels: 0
DB: 4 Gaps: 0

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US-10-649-952A-2 (1-501) x AAM78545 (1-166)

```

QY 1 ATGGCCCTCGGTGGCTGCTCTGATGCTGATCAAGGTGTTCAACGACATGAAGGTG 60
Db 1 MetAlaSerGlyValThrValAsnAspGluValIleLysValPheAsnAspMetLysVal 20
QY 61 CGTAAGTCTTCAACGCCAGAGGAGGTGAAGAGCGCAAGAGCGGTGCTCTTCGCTG 120
Db 21 ArgLysSerSerThrGlnGluGluIleLysLysArgLysLysAlaValLeuPheCysLeu 40
QY 121 AGTGAGGACCAAGAACATCATCTCGAGGAGGCAAGAGATCCTGTTGGGCGATGTG 180
Db 41 SerAspAspLysArgGlnIleValGluAlaLysGlnIleLysGlnIleValGlyAspIle 60
QY 181 GGCAGAGCTGTCAGCATCCTACGCCACCTTTGTCAGATGTCGCAGATAAGGACTGC 240
Db 61 GlyAspThrValGluAspProTyrThrSerPheValLysLeuLeuProLeuAsnAspCys 80
QY 241 CGCTATGCCCTCTATGATCAACCTATGAGACCAAGAGGAGGAGGAGGATCTGGT 300
Db 81 ArgTyrAlaLeuTyrAspAlaThrTyrGluThrLysGluSerLysLysGluAspLeuVal 100
QY 301 TTTATCTTCTGGGCCCCCGAGTCTGCGCCCTTAAGAGCAAAATGATTATGCCAGTCC 360
Db 101 PheIlePheTrpAlaProGluSerAlaProLeuLysSerLysMetIleTyrAlaSerSer 120
QY 361 AAGGAGCGCCATCAAGAAAGAGTGCAGGAGTCAAGCATGAATTGCAAGCAAACTGCTAC 420
Db 121 LysAspAlaIleLysLysLysPheThrGlyIleLysHisGluTrpGlnValAsnGlyLeu 140
QY 421 GAGGAGGTCAAGGACCGCTGCACCTCGCAGAGAGAGTGGGGGCGAGTGGCGTCACTCC 480
Db 141 AspAspIleLysAspArgSerThrLeuGlyGluLysLeuGlySerValValSer 160
QY 481 CTGAGGGCAAGCCTTTG 498
Db 161 LeuGluGlyLysProLeu 166

```


RESULT 12

ID ADB75248 standard; protein; 166 AA.
XX ADB75248;
AC ADB75248;
XX 04-DEC-2003 (first entry)
DT
XX Prostate cancer marker protein.
DE
XX Prostate; cancer; cytostatic; gene therapy; marker.
KW
XX Homo sapiens.
OS
XX WO2003009814-A2.
PN
XX 06-FEB-2003.
PD
XX 25-JUL-2002; 2002WO-US023913.
XX 25-JUL-2001; 2001US-0307982P.
XX 25-AUG-2001; 2001US-0314356P.
XX 25-SEP-2001; 2001US-0325020P.
XX 12-DEC-2001; 2001US-0341746P.
XX 05-MAR-2002; 2002US-0362158P.
XX (MILL-) MILLENNIUM PHARM INC.
XX Schlegel R, Monahan JE, Endege WO, Gannavarapu M, Gorbacheva B;
XX Hoersht S, Kamatkar S, Wonsay AM, Glat K, Zhao X, Anderson D;
XX WPI; 2003-248033/24.
XX New nucleic acid molecule, useful for diagnosing or treating prostate
XX cancer.
XX Disclosure; SEQ ID NO 72; 99pp; English.

The invention relates to newly discovered cancer markers associated with the cancerous state of prostate cells. Also disclosed is a method of assessing whether a patient is afflicted with prostate cancer. The method of the invention involves assessing whether a patient is afflicted with prostate cancer by comparing the level of expression of a marker in a patient sample and the normal level of expression of the marker in a control non-prostate cancer sample, where a significant increase in the level of expression of the marker in the patient sample and the normal level indicates that the patient is afflicted with prostate cancer. Nucleic acids of the invention are useful for diagnosing or treating prostate cancer, and may be useful in gene therapy. Sequences given in ADB75177-ADB75631 represent marker cDNA and proteins. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 166 AA;

Alignment Scores:
Pred. No.: 1.24e-66 Length: 166
Score: 699.00 Matches: 134
Percent Similarity: 89.76% Conservative: 15
Best Local Similarity: 80.72% Mismatches: 17
Query Match: 77.58% Indels: 0
DB: 7 Gaps: 0

US-10-649-952A-2 (1-501) x ADB75248 (1-166)

Qy 1 ATGGCTCCGTGGGTCTCTGTCATCAAGGTGTTCAACGACATGAAGTG 60
Db 1 MetAlaSerGlyValThrValAsnAspGluValIleLysValPheAsnAspMetLysVal 20
Qy 61 CGTAAGTCTTCAACGCCCAAGAGGTGAAGAGCGCGAGTGGTCTCTTCGCTG 120
Db 21 ArgLysSerSerThrGlnGluGluIleLysLysArgLysLysAlaValLeuPheCysLeu 40

Qy 121 AGTGAGGACAAGAACATCATCTGGAGGAGGCAAGAGATCCTGTGGCGCATGTG 180
Db 41 SerAspAspLysArgGlnIleIleValGluGluAlaLysGlnIleLeuValGlyAspIle 60
Qy 181 GGCAGACTCTCGACGATCCCTACGCCACCTTTGTCAAGATGTCGAGATAAGGACTGC 240
Db 61 GlyAspThrValGluAspProTyrThrSerPheValLysLeuLeuProLeuAsnAspCys 80
Qy 241 CGCTATGCCCTCTATGATGCAACCTATGACACCAAGGAGCAAGAGGAGGAGTCTCGTG 300
Db 81 ArgTyrAlaLeuTyrAspAlaThrTyrGluThrLysGluSerLysLysGluAspLeuVal 100
Qy 301 TTTATCTTCTGGGCCCGGAGTCTGCGCCCTTAAAGAGCAAAATGATTTATGCCAGTCC 360
Db 101 PheIlePheTrpAlaProGluSerAlaProLeuLysSerLysMetIleTyrAlaSerSer 120
Qy 361 AAGGACGCCATCAAGAAGAGCTGACAGGATCAAGCATCAATTCGAAGCAAACTGTCTAC 420
Db 121 LysAspAlaIleLysLysLysPheThrGlyIleLysHisGluTrpGlnValAsnGlyLeu 140
Qy 421 GAGGAGTCAAGGACCGCTGCACCCCTGGCAGAGAGCTGGGGGCGAGTGGCGTATCTCC 480
Db 141 AspAspIleLysAspArgSerThrLeuGlyLysLeuGlyLysLeuGlyAsnValValSer 160
Qy 481 CTGGAGGCAAGCCTTTG 498
Db 161 LeuGluGlyLysProLeu 166
RESULT 13
ADJ70104
ID ADJ70104 standard; protein; 166 AA.
XX AC ADJ70104;
XX DT
XX 06-MAY-2004 (first entry)
XX Human heat mitochondrial protein as a therapeutic target SeqID1910.
DE
XX Mitochondrial; human; screening assay; diabetes mellitus;
KW Huntington's disease; osteoarthritis;
KW Leber's hereditary optic neuropathy; LHON;
KW Mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
KW Myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
KW Neuroprotective; nontropic; antidiabetic; anticonvulsant; antiarthritic;
KW Osteopathic; ophthalmological; cytostatic.
XX
OS Homo sapiens.
XX
XX WO2003087768-A2.
PN
XX 23-OCT-2003.
PD
XX 04-APR-2003; 2003WO-US010870.
XX
XX 12-APR-2002; 2002US-0372843P.
XX 17-JUN-2002; 2002US-038987P.
XX 20-SEP-2002; 2002US-0412418P.
XX
XX (MITO-) MITOKOR.
XX (BUCK-) BUCK INST AGE RES.
XX
XX Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GW;
XX Warnock DE;
XX WPI; 2003-845369/78.
XX
XX Identifying a mitochondrial target for drug screening assays and for
XX treating diseases associated with altered mitochondrial function,
XX comprises detecting a modified polypeptide in a sample and correlating
XX with the disease.
XX
XX Claim 1; SEQ ID NO 1910; 180pp; English.
PS

XX This invention relates to novel mitochondrial targets that can be used
CC for therapeutic intervention in treating a disease associated with
CC altered mitochondrial function. Specifically, it refers to a method for
CC identifying proteins of the human heart mitochondrial proteome that are
CC useful for drug screening assays, as well as therapeutic targets. The
CC present invention describes a method for identifying such proteins that
CC can be used in the treatment of various diseases associated with altered
CC mitochondrial function including diabetes mellitus, Huntington's disease,
CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC compositions have neuroprotective, neurotropic, antidiabetic,
CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
CC cytostatic activities. This polypeptide sequence is a human heart
CC mitochondrial protein of the invention.

XX Sequence 166 AA;

Alignment Scores:
Pred. No.: 1,24e-66 Length: 166
Score: 699.00 Matches: 134
Percent Similarity: 89.76% Conservative: 15
Best Local Similarity: 80.72% Mismatches: 17
Query Match: 77.58% Indels: 0
DB: 7 Gaps: 0

US-10-649-952A-2 (1-501) x ADJ70104 (1-166)

QY 1 ATGGCTCCGGTGGCTGCTCTGATGCTCATCAGGTGTTCAACGACATGAAGGTG 60
Db 1 MetAlaSerGlyValThrValAsnAspGluValIleLysValPheAsnAspMetLysVal 20
QY 61 CGTAAGTCTTCAAGCCAGAGGAGGTGAAGAACGCAAGAGCGGTCTCTTCGCCCTG 120
Db 21 ArgLysSerSerThrGlnGluGluIleLysLysLysLysLysLysLysLysLysLysLys 40
QY 121 AGTGAGGACAAAGAACATCATCTCTGGAGGAGGCAAGAGATCTCTGGTGGCGGATGTG 180
Db 41 SerAspAspLysArgGlnIleValGluGluAlaLysGlnIleValGlyAspIle 60
QY 181 GGCAGACTGTCAAGATCCCTACGCCACCTTTGTCAAGATGTGCCAGATAAGGACTGC 240
Db 61 GlyAspThrValGluAspProTyrThrSerPheValLysLeuLeuProLeuAsnAspCys 80
QY 241 CGCTATGCCCTCTATGATGCAACTATGACACCAAGAGAGAGAGGAGGATCTGTG 300
Db 81 ArgTyrAlaLeuTyrAspAlaThrTyrGluThrLysGluSerLysLysLysLysLysLys 100
QY 301 TTATCTCTTGGGCCCCCGAGTCTGGCCCCCTTAAGAGCAAAATGATTATGCGAGCTCC 360
Db 101 PheIlePheThrAlaProGluSerAlaProLeuLysSerLysMetIleTyrAlaSerSer 120
QY 361 AAGAGCCCATCAAGAAAGAGTGTGACAGGATCAAGCATGAATTGCAAGCAAACTGCTAC 420
Db 121 LysAspAlaIleLysLysLysPheThrGlyIleLysHisGluTrpGlnValAsnGlyLeu 140
QY 421 GAGGAGGTCAAGACCGCTGCACCTCGGAGAGAGCTGGGAGAGAGTGGCGGAGTCTCTCC 480
Db 141 AspAspIleLysAspArgSerThrLeuGlyGluLysLeuGlyLysLysLysLysLysLys 160
QY 481 CTGGAGGGCAAGCCTTTG 498
Db 161 LeuGluGlyLysProLeu 166

RESULT 14
ADI24536

ID ADI24536 standard; protein; 166 AA.

XX

AC ADI24536;

XX

DT 15-APR-2004 (first entry)

XX

DE Human modifier of Chk1 (MCHK) protein SEQ ID NO:86.

XX Chk1 pathway modulating agent; modifier of Chk1; MCHK; cytostatic;
KW gene therapy; cancer; human.

XX Homo sapiens.

OS WO2004004785-A1.

PN 15-JAN-2004.

XX 09-JUL-2003; 2003WO-US021379.

XX 10-JUL-2002; 2002US-0394845P.

PR 16-SEP-2002; 2002US-0410986P.

XX (EXEL-) EXELIXIS INC.

XX Francis-Lang H, Roche S, Joo DM, Nicoll M, Hai B, Zhang H;
PI Lickteig K, Amundsen CD, Jin Y, Adamkewicz JI, Platt DM;
PI Hammonds RG;

XX WPI; 2004-083465/08.
DR N-PSDB; ADI24486.

XX Identifying a candidate Chk1 pathway modulating agent for treating e.g.,
PT cancer, comprises contacting an assay system comprising a MCHK
PT polypeptide or nucleic acid with a test agent and detecting a test agent-
PT biased activity.

XX Example; SEQ ID NO 86; 266pp; English.

XX The present invention describes a method for identifying a candidate Chk1
CC pathway modulating agent. The method comprises: (a) providing an assay
CC system comprising a modifier of Chk1 (MCHK) polypeptide or nucleic acid;
CC (b) contacting the system with a test agent, where the system provides a
CC reference activity except in the presence of the test agent; and (c)
CC detecting a test agent-biased activity, and a difference between the test
CC agent-biased activity and the reference activity. Also described: (1) a
CC method for modulating Chk1 pathway of a cell; (2) a method for modulating
CC Chk1 pathway in a mammalian cell; and (3) a method for diagnosing a
CC disease in a patient. A MCHK sequence has cytostatic activity, and can be
CC used in gene therapy. The method is useful for identifying a candidate
CC Chk1 pathway-modulating agent for preparing a composition for diagnosing
CC or treating e.g., cancer. The present sequence represents a human MCHK
CC protein, which is used in the exemplification of the present invention.

XX Sequence 166 AA;

Alignment Scores:
Pred. No.: 1,24e-66 Length: 166
Score: 699.00 Matches: 134
Percent Similarity: 89.76% Conservative: 15
Best Local Similarity: 80.72% Mismatches: 17
Query Match: 77.58% Indels: 0
DB: 8 Gaps: 0

US-10-649-952A-2 (1-501) x ADI24536 (1-166)

QY 1 ATGGCTCCGGTGGCTGCTCTGATGCTCATCAGGTGTTCAACGACATGAAGGTG 60
Db 1 MetAlaSerGlyValThrValAsnAspGluValIleLysValPheAsnAspMetLysVal 20
QY 61 CGTAAGTCTTCAAGCCAGAGGAGGTGAAGAACGCAAGAGCGGTCTCTTCGCCCTG 120
Db 21 ArgLysSerSerThrGlnGluGluIleLysLysLysLysLysLysLysLysLysLysLys 40
QY 121 AGTGAGGACAAAGAACATCATCTCTGGAGGAGGCAAGAGATCTCTGGTGGCGGATGTG 180
Db 41 SerAspAspLysArgGlnIleValGluGluAlaLysGlnIleValGlyAspIle 60
QY 181 GGCAGACTGTGAGGATCCCTACGCCACCTTTGTCAAGATGTGCCAGATAAGGACTGC 240

Db 61 GlyAspThrValGluAspProTyrThrSerPheValLysLeuLeuProLeuAsnAspCys 80
Qy 241 CGCTATGCCCTCTATGATGCAACCTATGAGACCAAGGAGAGCAAGAGGAGGATCTGGTG 300
Db 81 ArgTyrAlaLeuTyrAspAlaThrTyrGluThrLysGluSerLysGluAspLeuVal 100
Qy 301 TTTATCTTCTGGGCCCCGAGTCTGCGCCCTTAAGAGCAAAATGATTATGCGAGTCC 360
Db 101 PheIlePheTpaAlaProGluSerAlaProLeuLysSerLysMetIleTyrAlaSerSer 120
Qy 361 AAGACGCCATCAGAGCAAGCACTGACAGGATCAAGCATGATGATGCAAGCAAACTGCTAC 420
Db 121 LysAspAlaIleLysLysLysPheThrGlyIleLysHisGluTyrGlnValAsnGlyLeu 140
Qy 421 GAGGAGGTCAAGGACCGCTGACACCTGCAGAGAGCTGGGGGCGAGTGGGTCATCTCC 480
Db 141 AspAspIleLysAspArgSerThrLeuGlyLysLysGlyAsnValValSer 160
Qy 481 CTGGAGGCGCAAGCCTTTG 498
Db 161 LeuGluGlyLysProLeu 166
RESULT 15
AAU18546
ID AAU18546 standard; protein; 205 AA.
AC AAU18546;
XX
DT 21-NOV-2001 (first entry)
DE Human cytoskeletal element-related polypeptide #39.
KW Cytoskeletal element-related protein; human; mouse; rabbit; goat; horse;
cat; dog; chicken; sheep; immunosuppressive; antitharctic; vasotropic;
antirheumatic; antiproliferative; cytostatic; cardiant; neuroprotective;
cerebroprotective; nootropic; antibacterial; virucide; fungicide; cancer;
ophthalmological; vulnary; gene therapy; autoimmune disease; neoplasm;
hyperproliferative disorder; breast; liver; cardiovascular disorder;
cerebrovascular disorder; nervous system disorder; bacterial infection;
fungal infection; viral infection; ocular disorder; endocrine disorder;
gastrointestinal disorder; renal disorder; respiratory disorder;
wound healing; skin aging; organ transplantation; food preservative;
tissue regeneration; anti-infertility; food additive.
OS Homo sapiens.
XX
PN WO200155168-A1.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001331.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
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PR 14-JUL-2000; 2000US-0218290P.
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PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
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PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
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PR 14-AUG-2000; 2000US-0225758P.
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PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226868P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
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PR 01-SEP-2000; 2000US-0229287P.
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PR 01-SEP-2000; 2000US-0229344P.
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PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239335P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.

PR 08-NOV-2000; 2000US-0246524P.
 PR 08-NOV-2000; 2000US-0246525P.
 PR 08-NOV-2000; 2000US-0246526P.
 PR 08-NOV-2000; 2000US-0246527P.
 PR 08-NOV-2000; 2000US-0246528P.
 PR 08-NOV-2000; 2000US-0246532P.
 PR 08-NOV-2000; 2000US-0246609P.
 PR 08-NOV-2000; 2000US-0246610P.
 PR 08-NOV-2000; 2000US-0246611P.
 PR 08-NOV-2000; 2000US-0246613P.
 PR 17-NOV-2000; 2000US-0249207P.
 PR 17-NOV-2000; 2000US-0249208P.
 PR 17-NOV-2000; 2000US-0249209P.
 PR 17-NOV-2000; 2000US-0249210P.
 PR 17-NOV-2000; 2000US-0249211P.
 PR 17-NOV-2000; 2000US-0249212P.
 PR 17-NOV-2000; 2000US-0249213P.
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 PR 17-NOV-2000; 2000US-0249215P.
 PR 17-NOV-2000; 2000US-0249216P.
 PR 17-NOV-2000; 2000US-0249217P.
 PR 17-NOV-2000; 2000US-0249218P.
 PR 17-NOV-2000; 2000US-0249244P.
 PR 17-NOV-2000; 2000US-0249245P.
 PR 17-NOV-2000; 2000US-0249264P.
 PR 17-NOV-2000; 2000US-0249265P.
 PR 17-NOV-2000; 2000US-0249267P.
 PR 17-NOV-2000; 2000US-0249299P.
 PR 17-NOV-2000; 2000US-0249300P.
 PR 01-DEC-2000; 2000US-0250160P.
 PR 01-DEC-2000; 2000US-0250391P.
 PR 03-DEC-2000; 2000US-0251030P.
 PR 03-DEC-2000; 2000US-0251988P.
 PR 05-DEC-2000; 2000US-0256719P.
 PR 06-DEC-2000; 2000US-0251479P.
 PR 08-DEC-2000; 2000US-0251856P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251869P.
 PR 08-DEC-2000; 2000US-0251989P.
 PR 08-DEC-2000; 2000US-0251990P.
 PR 11-DEC-2000; 2000US-0254097P.
 PR 05-JAN-2001; 2001US-0259678P.
 (HUMA-) HUMAN GENOME SCI INC.
 Rosen CA, Barash SC, Ruben SM;
 WPI; 2001-476182/51.
 N-PSDB; AAS29808.

Novel isolated human cytoskeletal element-related polypeptide useful for diagnosis/treatment of neoplastic disorders, disorders associated with neural transmission, chromosomal abnormalities, autoimmune disorders.

Claim 11; SEQ ID NO 93; 505pp; English.

Sequences AAU18508-AAU18551 represent the cytoskeletal element-related polypeptides of the invention. Cytoskeletal polypeptides and their associated polynucleotides are useful in the diagnosis, treatment and prevention of various types of disorders in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. A pathological condition can be determined by determining the presence or absence of a mutation in a cytoskeletal polynucleotide. The treatable disorders include autoimmune diseases such as rheumatoid arthritis, hyperproliferative disorders such as neoplasms of the breast or liver, cardiovascular disorders such as cardiac arrest, cerebrovascular disorders such as cerebral ischaemia, nervous system disorders such as Alzheimer's disease, infections caused by bacteria, viruses and fungi, ocular disorders such as corneal infection, endocrine disorders such as premature labour and infertility, gastrointestinal disorders such as Crohn's disease, renal disorders such as glomerulonephritis and respiratory disorders such as asthma. The polypeptides can also be used to aid wound healing, to prevent skin aging due to sunburn, to maintain organs before transplantation, to regenerate

CC tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities.
 CC Note: The sequence data for this patent did not form part of the printed CC specification, but was obtained in electronic format directly from WIPO CC at ftp.wipo.int/pub/published_pct_sequences

Alignment Scores:
 Pred. No.: 1.33e-66 Length: 205
 Score: 699.00 Matches: 134
 Percent Similarity: 89.76% Conservative: 15
 Best Local Similarity: 80.72% Mismatches: 17
 Query Match: 77.58% Indels: 0
 DB: 4 Gaps: 0

US-10-649-952A-2 (1-501) x AAU18546 (1-205)

QY	1	ATGGCGCTCGGTGTGCTCTGATGCTGTCATCAAGGTGTTCAACGACATGAAGGTG	60
DB	40	MetAlaSerGlyValThrValAsnAspGluValLysValPheAsnAspMetLysVal	59
QY	61	CGTAAGTCTTCAACGCCAGAGGAGGTGAAGAGCGCAAGAGCGGTGCTCTTCTGCGCTG	120
DB	60	ArgLysSerSerThrGlnGluLulleLysLysArgLysLysAlaValLeuPheCysLeu	79
QY	121	AGTGAGGACAAGAACATCATCTCGAGGAGGCGAAGAGATCCTGGTGGCGGATGTG	180
DB	80	SerAspLysArgGlnLilleValGluAlaLysGlnLilleValGlyAspIle	99
QY	181	GGCCAGACTGTCGACGATCCCTAGCCACCTTTGTCAAGATGCTGCAGATAGGACTGC	240
DB	100	GlyAspThrValGluAspProTyrThrSerPheValLysLeuLeuProLeuAsnAspCys	119
QY	241	CGCTATGCCCTCTATGATCAACCTATGAGCAAGAGGAGCAAGAGGAGGATCTGGTG	300
DB	120	ArgTyrAlaLeuTyrAspAlaThrTyrGluThrLysGluSerLysLysGluAspLeuVal	139
QY	301	TTTATCTTCTGGGCCCCGAGTCTGGCCCCCTTTAAGAGCAAAATGATTTATGCAGCTCC	360
DB	140	PheIlePheTrpAlaProGluSerAlaProLeuLysSerLysMetIleTyrAlaSerSer	159
QY	361	AAGGAGCCATCAAGAGAGCTGACAGGATCAAGCATGATTTGCAAGCAAACTGCTAC	420
DB	160	LysAspAlaIleLysLysLysPheThrGlyIleLysHisGluTrpGlnValAsnGlyLeu	179
QY	421	GAGGAGGTCAAGGACCGCTGCACCTGGCAGAGAGCTGGGGGCGAGTCCGTCATCTCC	480
DB	180	AspAspIleLysAspArgSerThrLeuGlyGluLysLeuGlyGlyAsnValValSer	199
QY	481	CTGGAGGGCAAGCCTTTG	498
DB	200	LeuGluGlyLysProLeu	205

Search completed: May 13, 2005, 09:54:43
 Job time : 119.5 secs

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: May 13, 2005, 09:47:41 ; Search time 33.5 Seconds
(without alignments)
2877.886 Million cell updates/sec

Title: US-10-649-952A-2

Perfect score: 901

Sequence: 1 atggctccgggtggtgctgt.....tggagggaagcctttgtga 501

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO.spool_p/US10649952/runat_13052005_102649_27325/app_query.fasta_1.647
-DB=PIR -QMT=fastan -SUFFIX=n2p.rpr -MINMATCH=0.1 -LOOPCL=0 -IOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blowm62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pcp -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10649952@cgn 1.1 63 @runat_13052005_102649_27325 -NCPUs=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSFLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

1: PIR 79: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	846	93.9	166	1 S12632	cofilin - human
2	842	93.5	166	2 S49101	cofilin - rat
3	841	93.3	166	1 A29240	cofilin - pig
4	839	93.1	166	1 S12584	cofilin - mouse
5	702	77.9	166	2 A53812	cofilin, muscle -
6	701	77.8	166	1 B35703	cofilin - chicken
7	620.5	68.9	165	1 A35702	desrin - chicken
8	606.5	67.3	165	1 A35179	desrin - pig
9	606.5	67.3	165	1 A54184	desrin [validated
10	598.5	66.4	164	2 JE0223	desrin - rat
11	267.5	29.7	143	1 A44397	cofilin - yeast (S
12	254	28.2	137	2 T43245	probable actin-dep
13	227	25.2	139	2 T02914	actin-depolymerizi
14	213	23.6	140	2 A86149	actin-depolymerizi

15	208	23.1	132	2	G84717	actin depolymerizi
16	208	23.1	139	2	T02883	actin-depolymerizi
17	205.5	22.8	142	2	S71361	actin-binding prot
18	201.5	22.4	148	2	A57569	twinstar protein -
19	200.5	22.3	133	2	T01232	actin-depolymerizi
20	200.5	22.3	139	2	S30335	actin-depolymerizi
21	195.5	21.7	130	2	T47540	actin-depolymerizi
22	195	21.6	130	2	T05767	actin-depolymerizi
23	192.5	21.4	139	2	T02882	actin-depolymerizi
24	191	21.2	126	2	S30934	actin-depolymerizi
25	190.5	21.1	130	2	T05788	actin-depolymerizi
26	187	20.8	132	2	B84543	actin depolymerizi
27	185.5	20.6	135	2	T49327	cofilin related pr
28	176.5	19.6	58	2	A56448	actin-depolymerizi
29	158.5	17.6	133	2	T47539	actin-depolymerizi
30	157.5	17.5	49	2	B56448	cofilin-like prote
31	150.5	16.7	165	2	S41728	actin depolymerizi
32	149.5	16.6	293	2	T33952	actin depolymerizi
33	130	14.4	152	2	S41727	unc-60 protein - C
34	120	13.3	350	2	A59222	tyrosine kinase A6
35	104	11.5	349	2	T46362	probable tyrosine
36	102.5	11.4	221	2	C34768	ORF2 protein - Orf
37	101	11.2	200	2	S54834	HP8 peptide - huma
38	101	10.9	1958	2	B40505	hypothetical prote
39	98.5	10.9	358	2	T13017	hypothetical prote
40	98	10.9	328	2	T40910	probable tyrosine
41	97	10.5	1446	1	A45344	immediate-early pr
42	96.5	10.7	142	1	PT0410	glia maturation fa
43	96	10.7	141	1	JDB08	glia maturation fa
44	95.5	10.3	1460	1	EDBEIF	immediate-early pr
45	95	10.2	373	2	B75276	DNA-binding respon

ALIGNMENTS

RESULT 1

S12632

cofilin - human

C;Species: Homo sapiens (man)

C;Date: 03-Feb-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004

C;Accession: S12632

R;Ogawa, K.; Tashima, M.; Yumoto, Y.; Okuda, T.; Sawada, H.; Okuma, M.; Maruyama, Y.

Nucleic Acids Res. 18, 7169, 1990

A;Title: Coding sequence of human placenta Cofilin cDNA.

A;Reference number: S12632; MUID:91088330; PMID:2263493

A;Accession: S12632

A;Molecule type: mRNA

A;Residues: 1-166 <OGA>

A;Cross-references: UNIPROT:P23528; EMBL:D00682; NID:g219544; PIDN:BAA00589.1; PID:g21954

C;Comment: Cofilin reversibly regulates actin polymerization and depolymerization in a p

C;Genetics:

A;Gene: GDB:CFL1; CFL

A;Cross-references: GDB:126798; OMIM:601442

A;Map position: 11q13-11q13

C;Superfamily: cofilin

C;Keywords: actin binding; phosphoprotein

F;26-36/Region: nuclear location signal

F;104-134/Region: actin binding #status predicted

Alignment Scores:

Pred. No.: 1.33e-66 Length: 166
Score: 846.00 Matches: 166
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 93.90% Indels: 0
DB: 1 Gaps: 0

US-10-649-952A-2 (1-501) x S12632 (1-166)

QY 1 ATGGCTCCGGTGTGGCTCTCTGATGCTCATCAAGTGTTCACGACATGAGGTG 60

Db 1 MetAlaSerGlyValAlaValSerAspGlyValIleLysValPheAsnAspMetLysVal 20

Qy 61 CGTAAGTCTTCAACGCCAGAGAGGTGAAGAAGCGCAAGAGCGGTCTCTTCTGCTG 120
Db |||||||
Qy 121 AGTGAGGCAAGAAGAATCATCTCTGGAGGAGGCGCAAGAGATCTGTGGGCGATGTG 180
Db |||||||
Qy 181 GGCAGACTGTGAGGATCCCTAGCCACCTTTGTCAAGATGCTGCCAGATAAGGACTGC 240
Db |||||||
Qy 61 GlyGlnThrValAspSerProTyrAlaThrPheValLysMetLeuProAspLysAspCys 80
Qy 241 CGCTATGCCCTCTATGATGCAACCTATGAGACCAAGAGAGCAAGAAGGAGGATCTGTG 300
Db |||||||
Qy 81 ArgTyrAlaLeuTyrAspAlaThrTyrGluThrLysGluSerLysLysGluAspVal 100
Qy 301 TTTATCTTCTGGGCCCCGAGTCTGCGCCCTTAAAGAGCAAAATGATTATGCGCAGCTCC 360
Db |||||||
Qy 101 PheIlePheTyrAlaProGluSerAlaProLeuLysSerLysMetIleTyrAlaSerSer 120
Qy 361 AAGACGCCATCAGAAGAAGCTGACAGGATCAAGCATGAATTGCAAGCAAACTGCTAC 420
Db |||||||
Qy 121 LysAspAlaIleLysLysLysLeuThrGlyIleLysHisGluLeuGlnAlaAsnCysTyr 140
Qy 421 GAGGAGGTCAAGGACCGCTGCACCTGCGCAGAGAGCTGGGGGCGAGTGGCGGTCTCATCTCC 480
Db |||||||
Qy 141 GluGluValLysAspArgCysThrLeuAlaGluLysLeuGlyGlySerAlaValIleSer 160
Qy 481 CTGAGGCGCAAGCCTTTG 498
Db |||||||
Qy 161 LeuGluGlyLysProLeu 166

RESULT 2
S49101
cofilin - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Jan-1995 #sequence revision 12-May-1995 #text_change 09-Jul-2004
C:Accession: S49101; A58860; J0222
R:Shirahawa, T.; Takahashi, H.; Sakamoto, K.; Kawashima, A.; Akashi, T.
submitted to the EMBL Data Library, October 1991
A:Description: Nucleotide sequence of rat cofilin cDNA.
A:Reference number: S49101
A:Accession: S49101
A:Molecule type: mRNA
A:Residues: 1-166 <SH1>
A:Cross-references: UNIPROT:P45592; EMBL:X62908; NID:G509200; PIDN:CAA44694.1; PID:G50920
R:Shirahawa, T.
submitted to DDBJ, October 1991
A:Reference number: A58860
A:Accession: A58860
A:Molecule type: mRNA
A:Residues: 1-166 <SH2>
A:Cross-references: EMBL:X62908; NID:G509200; PIDN:CAA44694.1; PID:G509201
A:Experimental source: embryo brain
R:Kanamori, T.; Suzuki, M.M.; Titani, K.
submitted to JPIPD, August 1998
A:Description: Complete amino acid sequences and phosphorylation sites, determined by Ed
A:Reference number: J0222
A:Accession: J0222
A:Molecule type: protein
A:Residues: 2-166 <KAN>
C:Superfamily: cofilin
C:Keywords: acetylated amino end; phosphoprotein
F:2-166/Product: cofilin #status experimental <MAT>
F:19-34/Region: nuclear location signal
F:104-115/Region: actin binding #status predicted
F:2/Modified site: acetylated amino end (Ala) (in mature form) #status experimental
F:3/Binding site: phosphate (Ser) (covalent) #status experimental

Alignment Scores:
Pred. No.: 2.99e-66 Length: 166
Score: 842.00 Matches: 165
Percent Similarity: 99.40% Conservative: 0

Best Local Similarity: 99.40% Mismatches: 1
Query Match: 93.45% Indels: 0
DB: 2 Gaps: 0

US-10-649-952A-2 (1-501) x S49101 (1-166)

Qy 1 ATGGCCTCCGGTGGGTCTCTCTGATGGTGTCTCATCAAGGTGTTCACACGACATGAAGGTG 60
Db |||||||
Qy 1 MetAlaSerGlyValAlaValSerAspGlyValIleLysValPheAsnAspMetLysVal 20
Qy 61 CGTAAGTCTTCAACGCCAGAGGAGGTGAAGAAGCGCAAGAGCGGTCTCTTCTGCTG 120
Db |||||||
Qy 21 ArgLysSerThrProGluGluValLysLysArgLysLysAlaValLeuPheCysLeu 40
Qy 121 AGTGAGGCAAGAAGAATCATCTCTGGAGGAGGCGCAAGAGATCTGTGGGCGATGTG 180
Db |||||||
Qy 41 SerGluAspLysLysAsnIleLeuGluGluGlyLysGluIleLeuValGlyAspVal 60
Qy 181 GGCAGACTGTGCGACGATCCCTACGCCACCTTTGTCAAGATGCTGCCAGATAAGGACTGC 240
Db |||||||
Qy 61 GlyGlnThrValAspAspProTyrThrPheValLysMetLeuProAspLysAspCys 80
Qy 241 CGCTATGCCCTCTATGATGCAACCTATGAGACCAAGAGAGCAAGAAGGAGGATCTGTG 300
Db |||||||
Qy 81 ArgTyrAlaLeuTyrAspAlaThrTyrGluThrLysGluSerLysLysGluAspLeuVal 100
Qy 301 TTTATCTTCTGGGCCCCGAGTCTGCGCCCTTAAAGAGCAAAATGATTATGCGCAGCTCC 360
Db |||||||
Qy 101 PheIlePheTyrAlaProGluSerAlaProLeuLysSerLysMetIleTyrAlaSerSer 120
Qy 361 AAGGACGCCATCAGAAGAAGCTGACAGGATCAAGCATGAATTGCAAGCAAACTGCTAC 420
Db |||||||
Qy 121 LysAspAlaIleLysLysLysLeuThrGlyIleLysHisGluLeuGlnAlaAsnCysTyr 140
Qy 421 GAGGAGGTCAAGGACCGCTGCACCTGCGCAGAGAGCTGGGGGCGAGTGGCGGTCTCATCTCC 480
Db |||||||
Qy 141 GluGluValLysAspArgCysThrLeuAlaGluLysLeuGlyGlySerAlaValIleSer 160
Qy 481 CTGAGGCGCAAGCCTTTG 498
Db |||||||
Qy 161 LeuGluGlyLysProLeu 166

RESULT 3
A29240
cofilin - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 28-Aug-1989 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
R:Matsumoto, S.; Yahara, I.; Yonezawa, N.; Nishida, E.; Sakai, H.
J. Biol. Chem. 263, 11564-11568, 1988
A:Title: Cloning and characterization of porcine brain cofilin cDNA. Cofilin contains th
A:Reference number: A29240; MUID:88298817; PMID:3403546
A:Cross-references: UNIPROT:P10668; GB:M20866; NID:G164424; PIDN:AAA31020.1; PID:G164425
A:Residues: 1-166 <MAT>
A:Accession: A29240
A:Molecule type: mRNA
A:Cross-references: UNIPROT:P10668; GB:M20866; NID:G164424; PIDN:AAA31020.1; PID:G164425
C:Comment: Cofilin reversibly regulates actin polymerization and depolymerization in a p
C:Superfamily: cofilin
C:Keywords: actin binding; phosphoprotein
F:26-36/Region: nuclear location signal
F:104-134/Region: actin binding #status predicted

Alignment Scores:
Pred. No.: 3.67e-66 Length: 166
Score: 841.00 Matches: 165
Percent Similarity: 99.40% Conservative: 0
Best Local Similarity: 99.40% Mismatches: 1
Query Match: 93.34% Indels: 0
DB: 1 Gaps: 0

US-10-649-952A-2 (1-501) x A29240 (1-166)

Qy 1 ATGGCCTCCGGTGGGTCTCTCTGATGGTGTCTCATCAAGGTGTTCACACGACATGAAGGTG 60

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Db      1 MetAlaSerGlyValAlaValSerAspGlyValIleLysValPheAsnAspMetLysVal 20
Qy      61 CGTAAGTCTTCAACGCCAGAGGAGGTGAAGAAGCGCAAGAGCGGTGCTCTTCTGCGCTG 120
Db      21 ArgLysSerSerThrProGluGluValLysLysArgLysLysAlaValLeuPheCysLeu 40
Qy      121 AGTGAGACAAAGAAGAACATCATCTCTGGAGAGGCGCAAGAGATCTGGTGGCGATGTG 180
Db      41 SerGluAspLysLysAsnIleLeuGluGluGlyLysGluIleLeuValGlyAspVal 60
Qy      181 GGCAGACTCTCGACGATCCCTACGCCACCTTTGTCAAGATGCTGCAGATAAGGACTGC 240
Db      61 GlyGlnThrValAspAspProTyrThrPheValLysMetLeuProAspLysAspCys 80
Qy      241 CGCTATGCCCTCTATGATCAACCTATGAGACCAAGAGGAGCAAGAGGAGGATCTGGTG 300
Db      81 ArgTyrAlaLeuTyrAspAlaThrTyrGluThrLysGluSerLysLysGluAspLeuVal 100
Qy      301 TTTATCTTCTGGCCCCCGAGCTGCGCCCTTAAGAGCAAAATGATTTATGCGAGCTCC 360
Db      101 PheIlePheTrpAlaProGluCysAlaProLeuLysSerLysMetIleTyrAlaSerSer 120
Qy      361 AAGGACCCATCAAGAGAAGCTGACAGGATCAAGCATGAATTGCAAGCAAACTGCTAC 420
Db      121 LysAspAlaIleLysLysLysLeuThrGlyIleLysHisGluLeuGlnAlaAsnCysTyr 140
Qy      421 GAGGAGTCAAGGACCCCTGCAGAGAGCTGGGGGCGAGTGGGGTCACTCTCC 480
Db      141 GluGluValLysAspArgCysThrLeuAlaGluLysLeuGlySerAlaValIleSer 160
Qy      481 CTGAGGGCAAGCCTTTG 498
Db      161 LeuGluGlyLysProLeu 166

RESULT 4
S12584
Cofilin - mouse
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C;Accession: S12584; J00201
R;Moriyama, K.; Matsumoto, S.; Nishida, E.; Sakai, H.; Yahara, I.
Nucleic Acids Res. 18, 3053, 1990
A;Title: Nucleotide sequence of mouse cofilin cDNA.
A;Reference number: S12584; MUID:90272419; PMID:2349104
A;Accession: S12584
A;Molecule type: mRNA
A;Residues: 1-166 <MOR>
A;Cross-references: UNIPROT:P18760; EMBL:D00472; NID:G220383; PIDN:BA00364.1; PID:G2203
C;Comment: Cofilin reversibly regulates actin polymerization and depolymerization in a p
C;Superfamily: cofilin
F;28-36/Region: nuclear location signal
F;104-134/Region: actin binding #status predicted

Alignment Scores:
Pred. No.: 5 5e-66 Length: 166
Score: 839.00 Matches: 164
Percent Similarity: 99.40% Conservative: 1
Best Local Similarity: 98.80% Mismatches: 1
Query Match: 93.12% Indels: 0
DB: 1 Gaps: 0

US-10-649-952A-2 (1-501) x S12584 (1-166)

Qy      1 ATGGCTCCGGTGGGTGCTCTGATGGTGTATCAAGGTGTTCACGACATGAAGGTG 60
Db      1 MetAlaSerGlyValAlaValSerAspGlyValIleLysValPheAsnAspMetLysVal 20
Qy      61 CGTAAGTCTCAACGCCAGAGGAGGTGAAGAAGCGCAAGAGGATCTGGTGGCGATGTG 120
Db      21 ArgLysSerSerThrProGluGluValLysLysArgLysLysAlaValLeuPheCysLeu 40
Qy      121 AGTGAGACAAAGAAGAACATCATCTCTGGAGAGGCGCAAGAGATCTGGTGGCGATGTG 180
Db      41 SerGluAspLysLysAsnIleLeuGluGluGlyLysGluIleLeuValGlyAspVal 60
Qy      181 GGCAGACTCTCGACGATCCCTACGCCACCTTTGTCAAGATGCTGCAGATAAGGACTGC 240
Db      61 GlyGlnThrValAspAspProTyrThrPheValLysMetLeuProLeuAsnAspCys 80
Qy      241 CGCTATGCCCTCTATGATCAACCTATGAGACCAAGAGGAGCAAGAGGAGGATCTGGTG 300

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Qy      121 AGTGAGACAAAGAAGAACATCATCTCTGGAGAGGCGCAAGAGATCTGGTGGCGATGTG 180
Db      41 SerGluAspLysLysAsnIleLeuGluGluGlyLysGluIleLeuValGlyAspVal 60
Qy      181 GGCAGACTCTCGACGATCCCTACGCCACCTTTGTCAAGATGCTGCAGATAAGGACTGC 240
Db      61 GlyGlnThrValAspAspProTyrThrPheValLysMetLeuProAspLysAspCys 80
Qy      241 CGCTATGCCCTCTATGATCAACCTATGAGACCAAGAGGAGCAAGAGGAGGATCTGGTG 300
Db      81 ArgTyrAlaLeuTyrAspAlaThrTyrGluThrLysGluSerLysLysGluAspLeuVal 100
Qy      301 TTTATCTTCTGGCCCCCGAGCTGCGCCCTTAAGAGCAAAATGATTTATGCGAGCTCC 360
Db      101 PheIlePheTrpAlaProGluAsnAlaProLeuLysSerLysMetIleTyrAlaSerSer 120
Qy      361 AAGGACCCATCAAGAGAAGCTGACAGGATCAAGCATGAATTGCAAGCAAACTGCTAC 420
Db      121 LysAspAlaIleLysLysLysLeuThrGlyIleLysHisGluLeuGlnAlaAsnCysTyr 140
Qy      421 GAGGAGTCAAGGACCCCTGCAGAGAGCTGGGGGCGAGTGGGGTCACTCTCC 480
Db      141 GluGluValLysAspArgCysThrLeuAlaGluLysLeuGlySerAlaValIleSer 160
Qy      481 CTGAGGGCAAGCCTTTG 498
Db      161 LeuGluGlyLysProLeu 166

RESULT 5
A53812
Cofilin, muscle - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C;Accession: A53812
R;Ono, S.; Minami, N.; Abe, H.; Obinata, T.
J. Biol. Chem. 269, 15280-15286, 1994
A;Title: Characterization of a novel cofilin isoform that is predominantly expressed in
A;Reference number: A53812; MUID:94253093; PMID:8195165
A;Accession: A53812
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-166 <ONO>
A;Cross-references: UNIPROT:P45591; GB:L29468; NID:G498016; PIDN:AAA37433.1; PID:G498017
C;Superfamily: cofilin
C;Keywords: actin binding; muscle

Alignment Scores:
Pred. No.: 6 57e-54 Length: 166
Score: 702.00 Matches: 135
Percent Similarity: 89.76% Conservative: 14
Best Local Similarity: 81.33% Mismatches: 17
Query Match: 77.91% Indels: 0
DB: 2 Gaps: 0

US-10-649-952A-2 (1-501) x A53812 (1-166)

Qy      1 ATGGCTCCGGTGGGTGCTCTGATGGTGTATCAAGGTGTTCACGACATGAAGGTG 60
Db      1 MetAlaSerGlyValThrValAsnAspGluValIleLysValPheAsnAspMetLysVal 20
Qy      61 CGTAAGTCTTCAACGCCAGAGGAGGTGAAGAAGCGCAAGAGGATCTGGTGGCGATGTG 120
Db      21 ArgLysSerSerThrGlnGluLysLysLysArgLysLysAlaValLeuPheCysLeu 40
Qy      121 AGTGAGACAAAGAAGAACATCATCTCTGGAGAGGCGCAAGAGATCTGGTGGCGATGTG 180
Db      41 SerAspLysArgGlnIleIleValGluGluAlaLysGlnIleLeuValGlyAspIle 60
Qy      181 GGCAGACTCTCGACGATCCCTACGCCACCTTTGTCAAGATGCTGCAGATAAGGACTGC 240
Db      61 GlyAspThrValGluAspProTyrThrSerPheValLysLeuLeuProLeuAsnAspCys 80
Qy      241 CGCTATGCCCTCTATGATCAACCTATGAGACCAAGAGGAGCAAGAGGAGGATCTGGTG 300

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Db 81 ArgIyAlaLeuTyAspAlaThrTyGluThrIySgluSerIySgluAspLeuVal 100
Qy 301 TTTATCTCTGGGCCCCGAGCTGCGCCCTTAAGAGCAAAATGATTATGCCAGCTCC 360
Db 101 PheIlePheTrpAlaProGluSerAlaProLeuIySgluMetIleTyTyrAlaSer 120
Qy 361 AAGGACGCCATCAAGAAGACCTGACAGGGATCAAGCATGAATTGCAAGCAAACTGCTAC 420
Db 121 LysAspAlaIleIySgluPheThrGlyIleIySgluTrpGlnValAsnGlyLeu 140
Qy 421 GAGGAGTCAAGACCGCTGCACCTGCAGAGAGCTGGGGCAGTGGCGTCAATCTCC 480
Db 141 AspAspIleIySgluSerThrLeuGlyGluIySgluSerValValSer 160
Qy 481 CTGGAGGCAAGCCTTTG 498
Db 161 LeuGluGlyLysProLeu 166
RESULT 6
B35703
cofilin - chicken
C/Species: Gallus gallus (chicken)
C/Date: 12-Oct-1990 #sequence_revision 27-Jun-1994 #text_change 22-Jun-1999
C/Accession: B35703
R/Abel, H.; Endo, T.; Yamamoto, K.; Obinata, T.
Biochemistry 29, 7420-7425, 1990
A/Title: Sequence of cDNAs encoding actin depolymerizing factor and cofilin of embryonic
A/Reference number: A35703; MUID:91027755; PMID:1699599
A/Accession: B35703
A/Molecule type: mRNA
A/Residues: 1-166 <ABE>
A/Cross-references: GB:M55659; NID:g211569; PIDN:AAA62732.1; PID:g211570; GB:J02915
C/Comment: Cofilin reversibly regulates actin polymerization and depolymerization in a p
C/Keywords: actin binding; phosphoprotein
F:26-36/Region: nuclear location signal
F:104-134/Region: actin binding #status predicted
Alignment Scores:
Pred. No.: 8.04e-54 Length: 166
Score: 701.00 Matches: 135
Percent Similarity: 88.55% Conservative: 12
Best Local Similarity: 81.33% Mismatches: 19
Query Match: 77.80% Indels: 0
DB: 1 Gaps: 0
US-10-649-952A-2 (1-501) x B35703 (1-166)
Qy 1 ATGCGCTCCGTTGGTGTCTGATGGTGTCAAGGTGTCAAGCATCAAGGTG 60
Db 1 MetAlaSerGlyValThrValAsnAspGluValIleIySgluPheAsnAspMetLysVal 20
Qy 61 CGTAAGTCTTCAACGACAGAGAGGTGAAGAGCGCAAGAGCGGTCTCTTCTGCTG 120
Db 21 ArgIySerSerThrProGluIleIySgluSerIySgluValAlaValPheCysLeu 40
Qy 121 AGTGAGGCAAGAAGAACATCATCTCTGGAGAGGGCAAGGATCTTGGTGGCGATGTG 180
Db 41 SerAspAspIySgluIleValGluGluAlaThrArgIleLeuValGlyAspIle 60
Qy 181 GGCACAGATGTGAGGATCCCTAGCCACCTTTGTCAAGATGCTGCCAGATAAGGATGC 240
Db 61 GlyAspThrValGluAspProTyThrAlaPheValIySgluLeuProLeuAsnAspCys 80
Qy 241 CGCTATGCGCTCTATGATGCAACCTATGAGACCAAGGAGGAGGAGGATCTGGTG 300
Db 81 ArgIyAlaLeuTyAspAlaThrTyGluThrIySgluSerIySgluAspLeuVal 100
Qy 301 TTTATCTCTGGGCCCCGAGCTGCGCCCTTAAGAGCAAAATGATTATGCCAGCTCC 360
Db 101 PheIlePheTrpAlaProGluSerAlaProLeuIySgluMetIleTyTyrAlaSer 120

Qy 361 AAGGACGCCATCAAGAAGACCTGACAGGGATCAAGCATCAAGTTCAGCAAACTGCTAC 420
Db 121 LysAspAlaIleIySgluPheThrGlyIleIySgluTrpGlnValAsnGlyLeu 140
Qy 421 GAGGAGTCAAGACCGCTGCACCTGCAGAGAGCTGGGGCAGTGGCGTCAATCTCC 480
Db 141 AspAspIleIySgluSerThrLeuGlyGluIySgluSerValValSer 160
Qy 481 CTGGAGGCAAGCCTTTG 498
Db 161 LeuGluGlyLysProLeu 166
RESULT 7
A35702
desrin - chicken
N/Alternate names: actin-depolymerizing factor
C/Species: Gallus gallus (chicken)
C/Date: 12-Oct-1990 #sequence_revision 05-Aug-1994 #text_change 09-Jul-2004
C/Accession: A35702; A35703; A40672
R/Adams, M.E.; Minamide, L.S.; Duester, G.; Bamberg, J.R.
Biochemistry 29, 7414-7420, 1990
A/Title: Nucleotide sequence and expression of a cDNA encoding chick brain actin depolym
A/Reference number: A35702; MUID:91027754; PMID:2223773
A/Accession: A35702
A/Molecule type: mRNA
A/Residues: 1-165 <ADA>
A/Cross-references: UNIPROT:P18359; GB:J02912; NID:g211096; PIDN:AAA48575.1; PID:g211097
A/Experimental source: brain
A/Note: part of this sequence was confirmed by peptide sequencing
R/Abel, H.; Endo, T.; Yamamoto, K.; Obinata, T.
Biochemistry 29, 7420-7425, 1990
A/Title: Sequence of cDNAs encoding actin depolymerizing factor and cofilin of embryonic
A/Reference number: A35703; MUID:91027755; PMID:1699599
A/Accession: A35703
A/Molecule type: mRNA
A/Residues: 1-165 <ABE>
A/Cross-references: GB:M55660; GB:J02915; NID:g211092; PIDN:AAA48573.1; PID:g211093
A/Experimental source: muscle
A/Note: part of this sequence was confirmed by peptide sequencing
R/Morgan, T.E.; Lockerbie, R.O.; Minamide, L.S.; Browning, M.D.; Bamberg, J.R.
J. Cell Biol. 122, 623-633, 1993
A/Title: Isolation and characterization of a regulated form of actin depolymerizing fact
A/Reference number: A40672; MUID:93328764; PMID:7687605
A/Accession: A40672
A/Molecule type: protein
A/Residues: 20-30 <MOR>
R/Agnew, B.J.; Minamide, L.S.; Bamberg, J.R.
J. Biol. Chem. 270, 17582-17587, 1995
A/Title: Reactivation of phosphorylated actin depolymerizing factor and identification c
A/Reference number: A38989; MUID:9340558; PMID:7615584
A/Contents: annotation; acetylated amino end; phosphorylation site
C/Comment: Desrin is an actin-binding protein that is capable of rapidly depolymerizing
C/Superfamily: cofilin
C/Keywords: acetylated amino end; actin binding; phosphoprotein
F:2-165/Product: desrin #status predicted <MAR>
F:26-36/Region: nuclear location signal
F:104-134/Region: actin binding #status predicted
F:2/Modified site: acetylated amino end (Ala) (in mature form) #status experimental
F:3/Binding site: phosphate (Ser) (covalent) #status experimental
Alignment Scores:
Pred. No.: 1e-46 Length: 165
Score: 620.50 Matches: 122
Percent Similarity: 84.34% Conservative: 18
Best Local Similarity: 73.49% Mismatches: 25
Query Match: 68.87% Indels: 1
DB: 1 Gaps: 1
US-10-649-952A-2 (1-501) x A35702 (1-165)
Qy 1 ATGCGCTCCGTTGGTGTCTGATGGTGTCAAGGTGTTCACAGCATCAAGGTG 60


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Db 1 MetAlaSerGlyValGlnValAlaAspGluValCysArgIlePheTyrAspMetLysVal 20
|||||
QY 61 CGTAAGTCTTCAAGCCGAGAGGAGGTGAAGAAGCGCAAGAGCGGTCTCTTCTGCCTG 120
|||||
Db 21 ArgLysCysSerThrProGluGluValLysLysArgLysLysAlaValIlePheCysLeu 40
|||||
QY 121 AGTGAGGACAAGAAACATCATCTCTGGAGAGGCGCAAGAGATCTCTGGTGGCGATGTG 180
|||||
Db 41 SerProAspLysLysCysIleIleValGluGluGlyLysGluIleLeuValGlyAspVal 60
|||||
QY 181 GGCACAGCTCTCAGGATCCCTACGCCACCTTGTCAAGATGCTGCCAGATAAGGACTGC 240
|||||
Db 61 GlyValThrValThrAspProPheLysHisPheValGlyMetLeuProGluLysAspCys 80
|||||
QY 241 CGCTATGCTCTCTATGATCAACCTTATGACACCAAGAGAGGAGGAGGATCTGGTG 300
|||||
Db 81 ArgTyrAlaLeuTyrAspAlaSerPheGluThrLysGluSerLysLysGluGluLeuMet 100
|||||
QY 301 TTTATCTTCTGGCCCGGAGTCTGGCCCTTAAAGAGCAAAATGATTTATGCGAGCTCC 360
|||||
Db 101 PhePheLeuTrpAlaProGluGlnAlaProLeuLysSerLysMetIleTyrAlaSerSer 120
|||||
QY 361 AAGGAGCCATCAAGAGAGCTGACAGGATCAAGCATCAATTCGAAGCAAACTGCTAC 420
|||||
Db 121 LysAspAlaIleLysLysLysPheGlnGlyIleLysHisGluCysGlnAlaAsnGlyPro 140
|||||
QY 421 GAGGAGTCAAGGACCGCTGCACCTGGCAGAGAGCTGGGGGCGAGTGGCGTCATCTCC 480
|||||
Db 141 GluAspLeuAsnArgAlaCys---IleAlaGluLysLeuGlyGlySerLeuValAla 159
|||||
QY 481 CTGAGGGCAAGCCTTTG 498
|||||
Db 160 PheGluGlySerProVal 165
|||||

RESULT 8
A35179
destrin - pig
N;Alternate names: actin-depolymerizing factor
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 03-Aug-1990 #sequence_revision 05-Aug-1994 #text_change 09-Jul-2004
C;Accession: A35179
R;Moriyama, K.; Nishida, E.; Yonezawa, N.; Sakai, H.; Matsumoto, S.; Iida, K.; Yahara, I.
J. Biol. Chem. 265, 5768-5773, 1990
A;Title: Destrin, a mammalian actin-depolymerizing protein, is closely related to cofillin
A;Reference number: A35179; MUID:90202824; PMID:2156828
A;Accession: A35179
A;Molecule type: mRNA
A;Residues: 1-165 <MOR>
A;Cross-references: UNIPROT:P60982; GB:D90053; NID:G217681; PIDN:BAAL14105.1;
A;Experimental source: brain
C;Comment: Destrin is an actin-binding protein that is capable of rapidly depolymerizing
C;Superfamily: cofilin
C;Keywords: acetylated amino end; actin binding; phosphoprotein
F;2-165/Product: destrin #status predicted <MAT>
F;26-36/Region: nuclear location signal
F;104-134/Region: actin binding #status predicted
F;2/Modified site: acetylated amino end (Ala) (in mature form) #status predicted
F;3/Binding site: phosphate (Ser) (covalent) #status predicted

Alignment Scores:
Pred. No.: 1.72e-45 Length: 165
Score: 606.50 Matches: 118
Percent Similarity: 83.73% Conservative: 21
Best Local Similarity: 71.08% Mismatches: 26
Query Match: 67.31% Indels: 1
DB: 1 Gaps: 1

US-10-649-952A-2 (1-501) x A35179 (1-165)

QY 1 ATGGCTCGGTGGCTGCTCTGATGGTGTCATCAAGGTGTTCACGACATGAAGGTG 60
|||||
Db 1 MetAlaSerGlyValGlnValAlaAspGluValCysArgIlePheTyrAspMetLysVal 20
|||||
```

```
QY 61 CGTAAGTCTTCAAGCCGAGAGGAGGTGAAGAAGCGCAAGAGCGGTCTCTTCTGCCTG 120
|||||
Db 21 ArgLysCysSerThrProGluGluIleLysLysArgLysLysAlaValIlePheCysLeu 40
|||||
QY 121 AGTGAGGACAAGAAACATCATCTCTGGAGAGGCGCAAGAGATCTCTGGTGGCGATGTG 180
|||||
Db 41 SerAlaAspLysLysCysIleIleValGluGluGlyLysGluIleLeuValGlyAspVal 60
|||||
QY 181 GGCACAGCTCTCAGGATCCCTACGCCACCTTGTCAAGATGCTGCCAGATAAGGACTGC 240
|||||
Db 61 GlyValThrIleThrAspProPheLysHisPheValGlyMetLeuProGluLysAspCys 80
|||||
QY 241 CGCTATGCTCTCTATGATCAACCTTATGACACCAAGAGAGGAGGAGGATCTGGTG 300
|||||
Db 81 ArgTyrAlaLeuTyrAspAlaSerPheGluThrLysGluSerLysLysGluGluLeuMet 100
|||||
QY 301 TTTATCTTCTGGCCCGGAGTCTGGCCCTTAAAGAGCAAAATGATTTATGCGAGCTCC 360
|||||
Db 101 PhePheLeuTrpAlaProGluGluAlaProLeuLysSerLysMetIleTyrAlaSerSer 120
|||||
QY 361 AAGGAGCCATCAAGAGAGCTGACAGGATCAAGCATCAATTCGAAGCAAACTGCTAC 420
|||||
Db 121 LysAspAlaIleLysLysLysPheGlnGlyIleLysHisGluCysGlnAlaAsnGlyPro 140
|||||
QY 421 GAGGAGTCAAGGACCGCTGCACCTGGCAGAGAGCTGGGGGCGAGTGGCGTCATCTCC 480
|||||
Db 141 GluAspLeuAsnArgAlaCys---IleAlaGluLysLeuGlyGlySerLeuIleValAla 159
|||||
QY 481 CTGAGGGCAAGCCTTTG 498
|||||
Db 160 PheGluGlyCysProVal 165
|||||

RESULT 9
A54184
destrin [validated] - human
N;Alternate names: actin-depolymerizing factor (ADF)
C;Species: Homo sapiens (man)
C;Date: 13-Sep-1994 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C;Accession: A54184
R;Hawkins, M.; Pope, B.; Maciver, S.K.; Weeds, A.G.
Biochemistry 32, 9985-9993, 1993
A;Title: Human actin depolymerizing factor mediates a pH-sensitive destruction of actin
A;Reference number: A54184; MUID:94002009; PMID:8399167
A;Accession: A54184
A;Molecule type: mRNA
A;Residues: 1-165 <HAW>
A;Cross-references: UNIPROT:P60981; GB:S65738; NID:G415586; PIDN:AAB28361.1; PID:G415587
A;Experimental source: fetal brain
A;Note: sequence extracted from NCBI backbone (NCBI:137963, NCBI:137964)
R;Hatanaka, H.; Moriyama, K.; Ogura, K.; Ichikawa, S.; Yahara, I.; Inagaki, F.
submitted to the Brookhaven Protein Data Bank, May 1997
A;Reference number: A67992; PDB:1AK6
A;Contents: annotation; conformation by (1)H-, (13)C-, and (15)N-NMR, residues 'TMTPSSG
R;Hatanaka, H.; Ogura, K.; Moriyama, K.; Ichikawa, S.; Yahara, I.; Inagaki, F.
Cell 85, 1047-1055, 1996
A;Title: Tertiary structure of destrin and structural similarity between two actin-regula
A;Reference number: A38990; MUID:96270507; PMID:8674111
A;Contents: annotation; NMR
C;Comment: The unphosphorylated form of destrin is capable of rapidly depolymerizing F-act
C;Genetics:
A;Gene: GDB:ACTDP
A;Cross-references: GDB:249179
C;Superfamily: cofilin
C;Keywords: acetylated amino end; actin binding; phosphoprotein
F;2-165/Product: destrin #status predicted <MAT>
F;26-36/Region: nuclear location signal
F;104-134/Region: actin binding #status predicted
F;2/Modified site: acetylated amino end (Ala) (in mature form) #status predicted
F;3/Binding site: phosphate (Ser) (covalent) #status predicted

Alignment Scores:
Pred. No.: 1.72e-45 Length: 165
Score: 606.50 Matches: 118
Percent Similarity: 83.73% Conservative: 21
Best Local Similarity: 71.08% Mismatches: 26
Query Match: 67.31% Indels: 1
DB: 1 Gaps: 1
```

Score: 606.50 Matches: 118
Percent Similarity: 83.73% Conservative: 21
Best Local Similarity: 71.08% Mismatches: 26
Query Match: 67.31% Indels: 1
DB: 1 Gaps: 1

US-10-649-952A-2 (1-501) x A54184 (1-165)

QY 1 ATGGCCCTCGGTGGCTGCTCTGATGGTGTCTCATCAAGGTGTTCAACGACATCAAGGTG 60
DB 1 MetAlaSerGlyValGlnValAlaAspGluValCysArgIlePheTyrAspMetLysVal 20
QY 61 CGTAAGTCTTCAACGCCAGAGAGGTGAAGAGCGCAAGAGCGCGTCTCTTCGCTG 120
DB 21 ArgLysCysSerThrProGluGluIleLysLysArgLysLysAlaValIlePheCysLeu 40
QY 121 AGTGAAGACAAGACAATCATCTCTGAGAGGGCAAGAGATCTCTGGGGCGATGTG 180
DB 41 SerAlaAspLysLysCysIleIleValGluGluGlyLysGluIleLeuValGlyAspVal 60
QY 181 GSCCAGACTGTCGAGCATCCTACGCCACCTTCTCAAGATGCTGCCAGATAAGGACTGC 240
DB 61 GlyValThrIleThrAspProPheLysHisPheValGlyMetLeuProGluLysAspCys 80
QY 241 CGCTATGCTCTATGATCAACCTATGACACCAAGAGAGCAAGAGAGGATCTGGTG 300
DB 81 ArgTyrAlaLeuTyrAspAlaSerPheGluThrLysGluSerArgLysGluGluLeuMet 100
QY 301 TTTATCTTCTGGGCCCGGAGCTGCGCCCTTAAGAGCAAAATGATTATGCGAGCTCC 360
DB 101 PhePheLeuTyrAlaProGluLeuAlaProLeuLysSerLysMetIleTyrAlaSerSer 120
QY 361 AAGCAGCGCATCAAGAGAAGCTCACAGGGATCAAGCATGAATGCAAGCAAACTGCTAC 420
DB 121 LysAspAlaIleLysLysLysPheGlnGlyIleLysHisGluCysGlnAlaAsnGlyPro 140
QY 421 GAGGAGGTCAAGGACCGCTGCACCTCGCAGAGAGCTGGGGGCGAGTGGCGTTCATCTCC 480
DB 141 GluAspLeuAsnArgAlaCys--IleAlaGluLysLeuGlyGlySerLeuIleValAla 159
QY 481 CTGAGGCAAGCCTTTG 498
DB 160 PheGluGlyCysProVal 165

RESULT 10

destrin - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 09-Jul-2004
C:Accession: J0223
R:Kanamori, T.; Suzuki, M.M.; Titani, K.
submitted to JPIB, August 1998
A:Description: Complete amino acid sequences and phosphorylation sites, determined by Ed
A:Reference number: J0222
A:Accession: J0223
A:Molecule type: protein
A:Residues: 1-164 <KAN>
A:Cross-references: UNIPROT:Q7M0E3
C:Superfamily: coflin
C:Keywords: acetylated amino end; phosphoprotein
F:18-33/Region: nuclear location signal
F:103-114/Region: actin binding #status predicted
F:1/Modified site: acetylated amino end (Ala) #status experimental
F:2/Binding site: phosphate (Ser) (covalent) #status experimental

Alignment Scores:
Pred. No.: 8.72e-45 Length: 164
Score: 598.50 Matches: 115
Percent Similarity: 84.24% Conservative: 24
Best Local Similarity: 69.70% Mismatches: 25
Query Match: 66.43% Indels: 1
DB: 2 Gaps: 1

US-10-649-952A-2 (1-501) x JE0223 (1-164)

QY 4 GCCTCCGCTGGCTGCTCTGATGGTGTCTCATCAAGGTGTTCAACGACATCAAGGTGCGT 63
DB 1 AlaSerGlyValGlnValAlaAspGluValCysArgIlePheTyrAspMetLysValArg 20
QY 64 AAGTCTTCAACGCCAGAGAGGTGAAGAGCGCAAGAGCGGTCTCTTCTGCTGAGT 123
DB 21 LysCysSerThrProGluGluIleLysLysArgLysLysAlaValIlePheCysLeuSer 40
QY 124 GAGGACAAGACAATCATCTCTGAGAGGGCAAGAGATCTCTGGGGCGATGTGGGC 183
DB 41 AlaAspLysLysCysIleIleValGluGluGlyLysGluIleLeuValGlyAspValGly 60
QY 184 CAGACTGTCGACCATCTACGCCACCTTGTCAAGATGCTGCCAGATAAGGACTGCGCG 243
DB 61 ValThrIleThrAspProPheLysHisPheValGlyMetLeuProGluLysAspCysArg 80
QY 244 TATGCCCTCTATGATCAACCTATGACACCAAGAGAGCAAGAGGATCTGGTGTGTTT 303
DB 81 TyrAlaLeuTyrAspAlaSerPheGluThrLysGluSerArgLysGluGluLeuMetPhe 100
QY 304 ATCTTCTGGGCCCGGAGCTGCGCCCTTAAGAGCAAAATGATTATGCGAGCTCCAAG 363
DB 101 PheLeuTyrAlaProGluGlnAlaProLeuLysSerLeuMetIleTyrAlaSerSerLys 120
QY 364 GAGCCATCAAGAGAAGCTGACAGGGATCAAGCATGAATGCAAGCAAACTGCTACGAG 423
DB 121 AspAlaIleLysLysLysPheProGlyIleLysHisGluTyrGlnAlaAsnGlyProGlu 140
QY 424 GAGTCAAGCAGCTGCACCTCGCAGAGAGCTGGGGGCGAGTGGCGTTCATCTCCCTG 483
DB 141 AspLeu--AsnArgThrSerIleAlaGluLysLeuGlyGlySerLeuIleValAlaPhe 159
QY 484 GAGGCAAGCCTTTG 498
DB 160 GluGlySerProVal 164

RESULT 11

A44397
Cofflin - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein I0595; protein YLL050c
C:Species: Saccharomyces cerevisiae
C:Date: 31-Dec-1993 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C:Accession: A44397; B44397; JN0529; S64802; S50970; S31309; S36087
R:Moore, A.L.; Jamney, P.A.; Louie, K.A.; Drubin, D.G.
J. Cell Biol. 120, 421-435, 1993
A:Title: Cofflin is an essential component of the yeast cortical cytoskeleton.
A:Reference number: A44397; MUID:93132073; PMID:8421056
A:Accession: A44397
A:Molecule type: DNA
A:Residues: 1-143 <MOO>
A:Cross-references: UNIPROT:Q03048; EMBL:Z14971; NID:93563; PIDN:CAA78594.1; PID:93564
A:Note: sequence extracted from NCBI backbone (NCBIN:122683, NCBI:122684)
A:Accession: B44397
A:Molecule type: protein
A:Residues: 43-56; 83-96, 'X', 98-106-129, 'DS', 132-141 <MO2>
A:Note: sequence extracted from NCBI backbone
R:Iida, K.; Moriyama, K.; Matsumoto, S.; Kawasaki, H.; Nishida, E.; Yahara, I.
Gene 124, 115-120, 1993
A:Title: Isolation of a yeast essential gene, COF1, that encodes a homologue of mammalia
A:Reference number: JN0529; MUID:93178959; PMID:8440472
A:Accession: JN0529
A:Molecule type: DNA
A:Residues: 1-143 <IID>
A:Cross-references: GB:D13230; NID:9287599; PIDN:BAA02514.1; PID:g287600
R:Wedler, H.; Wedler, E.; Scharfe, M.; Wambutt, R.
submitted to the Protein Sequence Database, May 1996
A:Reference number: S64792
A:Accession: S64802
A:Molecule type: DNA
A:Residues: 1-143 <WED>
A:Cross-references: EMBL:Z73155; NID:g1360250; PIDN:CAA97502.1; PID:g1360251; GSPDB:GN00

A;Note: experimental_source strain S288C
R;Medler, H.; Wambutt, R.
submitted to the EMBL Data Library, January 1995
A;Description: Sequence of a 37 kb DNA fragment from chromosome XII of *Saccharomyces cerevisiae*
A;Reference number: S50950
A;Accession: S50970
A;Molecule type: DNA
A;Residues: 'MWGKKFIRSQNVKFLCS', 6-143 -NEW>
A;Cross-references: EMBL:Z47973; NID:G642313; PIDN:CAA88007.1; PID:G642334
C;Comment: Cofilin reversibly regulates actin polymerization and depolymerization in a p
C;Genetics:
A;Gene: SGD:COF1; MIPS:YLL050C
A;Cross-references: SGD:S0003973; MIPS:YLL050C
A;Map position: 12L
A;Introns: 5/2
C;Superfamily: cofilin
C;Keywords: actin binding
P;88-118/Region: actin binding #status predicted

Alignment Scores:
Pred. No.: 1.31e-15 Length: 143
Score: 267.50 Matches: 54
Percent Similarity: 59.44% Conservative: 31
Best Local Similarity: 37.76% Mismatches: 37
Query Match: 29.69% Indels: 21
DB: 1 Gaps: 3

US-10-649-952A-2 (1-501) x A44397 (1-143)

Qy 7 TCCGGTGGCTGCTCTCTGATGGTGTCATCAAGGTGTTCAACGACATGAAGTGGCGTAAG 66
Db 4 SerGlyValAlaValAlaAspGluSerLeuThrAlaPheAsnAspLeuLys----- 20
Qy 67 TCTTCAACGCCACAGGAGGTGAAGAAGCGCAAGAAGCGCGGTGCTCTTCTGCCGTGAGTGAG 126
Db 21 -----LeuGlyLysLysTyLysPheIleuPheGlyLeuAsnAsp 34
Qy 127 GACAAGAAGAACATCATCTCTGGAGGAGGGCAAGGAGATCTCTGTGGCGCATGTGGGCCAG 186
Db 35 AlaLysThrGluIleValLysGlu-----Thr 44
Qy 187 ACTGTGCAGCATCCCTACGCCACCTTTGTCAAGATGCTGCCAGATAAGACTGCCCTAT 246
Db 45 SerThrAspProSerTyAspAlaPheLeuGlyLysLeuProGluAsnAspCysLeuTyr 64
Qy 247 GCCTCTATCATGCAACCTATGAGACC-----AAGGAGCAAGAGGAGGATCTGGTG 300
Db 65 AlaIleTyAspPheGluTyGluIleAsnGlyAsnGlyLysArgSerLysIleVal 84
Qy 301 TTTATCTTCTGGGCCCCCGAGTCTGGCCCTTTAAGACAAATGATTTATGCGACTCC 360
Db 85 PhePheThrTrpSerProAspThrAlaProValArgSerLysMetValTyAlaSerSer 104
Qy 361 AAGACGCCATCAAGAAGAGCTGCACAGGATCAGCATGAATGCAAGCAAACTGCTAC 420
Db 105 LysAspAlaLeuArgAlaLeuAsnGlyValSerThrAspValGlnGlyThrAspPhe 124
Qy 421 GAGGAGGTC 429
Db 125 SerGluVal 127

RESULT 12
T43245
probable actin-depolymerizing factor - fission yeast (*Schizosaccharomyces pombe*)
C;Species: *Schizosaccharomyces pombe*
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T43245; T38120
R;Kawamukai, M.
submitted to the EMBL Data Library, December 1996
A;Description: S. pombe cDNA for actin depolymerizing factor.
A;Reference number: Z23362
A;Accession: T43245
A;Status: preliminary; translated from GB/EMBL/DDBY

A;Molecule type: mRNA
A;Residues: 1-137 <RAW>
A;Cross-references: UNIPROT:P78929; EMBL:D89939; PIDN:BAAL4039.1
R;Connor, R.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, August 1996
A;Reference number: Z21771
A;Accession: T38120
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-137 <CON>
A;Cross-references: EMBL:Z98600; PIDN:CAB11258.1; GSPDB:GN00066; SPDB:SPAC20G4.06c
A;Experimental source: strain 972h-; cosmid c20G4
C;Genetics:
A;Gene: SPAC20G4.06c
A;Map position: 1
A;Introns: 1/3; 37/1
A;Note: adf1
C;Superfamily: cofilin
C;Keywords: actin binding

Alignment Scores:
Pred. No.: 2,02e-14 Length: 137
Score: 254.00 Matches: 53
Percent Similarity: 58.94% Conservatives: 36
Best Local Similarity: 35.10% Mismatches: 42
Query Match: 28.19% Indels: 20
DB: 2 Gaps: 3

US-10-649-952A-2 (1-501) x T43245 (1-137)

Qy	7	TCGGTGTGGCTGTCTCTGATGGTGTCTCAAGAGTGTTCACGACACATGAAGTGGCGTAAG	66
Db	4	SerGlyValIysValSerProGluCysLeuGluAlaPheGlnGluLeuIysLeuGlyLys	23
Qy	67	TCTTCAACGCCAGAGAGGTGAAGACCCAGAGACGGCGTGCTCTTCCTGCCTGAGTGAG	126
Db	24	Ser-----LeuArgTyrValValPheLysMetAsnAsp	34
Qy	127	GACAAAGAAGACATCATCTCGAGGAGGGCAAGGAGATCTGTGGCGCATGTGGGCCAG	186
Db	35	ThrLysThrGluIleValValGluLys-----Lys	44
Qy	187	ACTGTCGACGATCCCTCAAGCCACCTTTGTCAAGATGCTGCCAGATAAGGACTGCCGCTAT	246
		:::	
Db	45	SerThrAspLysAspPheAspThrPheLeuGlyAspLeuProGluLysAspCysArgTyr	64
Qy	247	GCCTCTATGATGCACACCTATGAGACCAGGAGGACGACGAGGAGGATCTGCTGTTTATC	306
Db	65	AlaIleTyrAspPheGluPheAsnLeuGlyGluValArgAsnLysIleIlePheIle	84
Qy	307	TTCTGGGCCCCGAGTCTCGCCCTTAAGAGCAAAATGATTTATGCCAGTCCCAAGGAC	366
Db	85	SerTrpSerProAspValAlaProIleLysSerLysMetValTyrSerSerLysAsp	104
Qy	367	GCCATCAAGAAGAAGCTGACGGGATCAAGCATGAATTCACAGCAAACTGCTACGAGGAG	426
		:::	
Db	105	ThrLeuArgArgAlaPheThrGlyIleGlyThrAspIleGlnAlaThrAspPheSerGlu	124
Qy	427	GTCACGACCGGTGCACCTCGCAGAGAGCTG	459
Db	125	ValAlaTyrGlu---ThrValLeuGluLysVal	134

RESULT 13
T02914
actin-depolymerizing factor 3 - maize
C;Species: Zea mays (maize)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C;Accession: T02914
R;Lopez, I.; Anthony, R.G.; Maciver, S.K.; Jiang, C.J.; Khan, S.; Weeds, A.G.; Huse
Proc. Natl. Acad. Sci. U.S.A. 93, 7415-7420, 1996
A;Title: Pollen specific expression of maize genes encoding actin depolymerizing fa
A;Reference number: Z14757; MUID:96293540; PMID:8693008
A;Accession: T02914

T43245
probable actin-depolymerizing factor - fission yeast (*Schizosaccharomyces pombe*)
C;Species: *Schizosaccharomyces pombe*
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T43245; T38120
R;Kawamukai, M.
submitted to the EMBL Data Library, December 1996
A;Description: S. pombe cDNA for actin depolymerizing factor.
A;Reference number: Z22362
A;Accession: T43245
A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-139 <LOP>

A;Cross-references: UNIPROT:Q41764; EMBL:X97726; NID:gl419369; PIDN:CAA66311.1; PID:gl4141

A;Experimental source: leaf

C;Genetics:

A;Gene: ABP3

C;Superfamily: cofilin

C;Keywords: actin binding

Alignment Scores:

Pred. No.:	4.85e-12	Length:	139
Score:	227.00	Matches:	54
Percent Similarity:	54.00%	Conservative:	27
Best Local Similarity:	36.00%	Mismatches:	45
Query Match:	25.19%	Indels:	24
DB:	2	Gaps:	5

US-10-649-952A-2 (1-501) x T02914 (1-139)

Qy	7	TCCGGTGGCTGCTCTCATCAAGGTGTCATCAAGGTGTTCAACGACATGAAGTGGTAAG	66
Db	6	SerGlyValAlaValAsnAspGluCysMetLeuLysPheGlyGluLeu	21
Qy	67	TCTTCAAGCCGACAGGAGGTCAAGAGCCCAAGAGCGGCTCTCTGCTCGCTGAGTGAG	126
Db	22	-----GlnSerLysArgLeuHisargPheIleThrPheLysMetAspAsp	36
Qy	127	GACAAGAAGACATCTCTCGAGAGGAGGCAAGAGATCTCTGGTGGCGATGGGGCCAG	186
Db	37	LysPheLysGluIleValValAspGln-----ValGlyAspArgAlaThr	51
Qy	187	ACTGTGACGATCCCTAGCCACCTTCTCAAGATGCTGCCAGATAGGATGCGCTAT	246
Db	52	SerTyrAspAsp-----PheThrAsnSerLeuProGluAsnAspCysArgTyr	67
Qy	247	CCCTCTATGATCAACCTATGACACCAAGAGAGAGC---AAGAAGGAGGATCTGCTTT	303
Db	68	AlaIleTyrAspPheAppPheValThrAlaGluAspValGlnLysSerArgIlePheTyr	87
Qy	304	ATCTTCTGGGCCCCGAGTCTGGCCCCCTTAAGAGCAAAATGATTATGCGAGTCCAAG	363
Db	88	IleLeuTyrSerProSerSerAlaLysValLysSerLysMetLeuTyrAlaSerSerAsn	107
Qy	364	GACCCATCAGAGAGAGCTCAGAGGATCAGCATGAATTCAGCAAGCAAC-----	414
Db	108	GlnLysPheLysSerGlyLeuAsnGlyIleGlnValGluLeuGlnAlaThrAspAlaSer	127
Qy	415	-----TGCTACGAGGAGGTCAAGACCGC	438
Db	128	GluIleSerLeuAspGluIleLysAspArg	137

RESULT 14

A86149
actin-depolymerizing factor homolog At1g01750 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: A86149
R;Theologos, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: A86149
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-140 <STO>

A;Cross-references: UNIPROT:Q9LQ81; GB:AE005172; NID:98671845; PIDN:AAF78408.1; GSPDB:GN1
C;Genetics:
A;Map position: 1
C;Superfamily: cofilin

Alignment Scores:

Pred. No.:	8.32e-11	Length:	140
Score:	213.00	Matches:	50
Percent Similarity:	57.14%	Conservative:	38
Best Local Similarity:	32.47%	Mismatches:	42
Query Match:	23.64%	Indels:	24
DB:	2	Gaps:	5

US-10-649-952A-2 (1-501) x A86149 (1-140)

Qy	4	GCCTCCGGTGGCTGCTCTCATCAAGGTGTCATCAAGGTGTTCAACGACATGAAGTGGT	63
Db	5	AlaSerGlyMetHisValSerAspGluCysLysLeuLysPheLeuGluLeuLys-----	22
Qy	64	AAGTCTTCAAGCCGACAGGAGGTGAAGAACGCAAGAGCGGCTCTCTGCTCGT	123
Db	23	-----AlaLysArgAsnTyrArgPheIleValPheLysIleAsp	35
Qy	124	GAGCACAAGAAGAACATCATCTCGAGAGGAGGCAAGAGATCTCTGGTGGCGATGGGC	183
Db	36	GluLysAlaGlnGlnValMetIleAspLys-----LeuGlyAsnProGlu	50
Qy	184	CAGATCTCCAGCATCCCTAGCCACCTTCTCAAGATGCTGCCAGATAGGACTGGCGC	243
Db	51	GluThrTyrGluAsp-----PheThrArgSerIleProGluAspGluCysArg	66
Qy	244	TATGCCCTCTATGATCAACCTATGACACCAAGAGAGC---AAGAAGGAGGATCTGCTG	300
Db	67	TyrAlaValIleTyrAspTyrAspPheThrProGluAsnCysGlnLysSerLysIlePhe	86
Qy	301	TTTATCTTCTGGCCCCGAGTCTGGCCCCCTTAAGAGCAAAATGATTATGCGAGTCC	360
Db	87	PheIleAlaIleTyrSerProAspThrSerArgValArgSerLysMetLeuTyrAlaSer	106
Qy	361	AAGACGCCATCAAGAAGAAGCTCAGAGGATCAGCATGAATTCAGCAAGCAAACTGCTAC	420
Db	107	LysAspArgPheLysArgGluLeuAspGlyIleGlnValGluLeuGlnAlaThrAspPro	126
Qy	421	GAGGAG-----GTCAAGGACGCTGACACCTG	447
Db	127	SerGluMetSerLeuAspIleIleLysGlyArgValAsnLeu	140

RESULT 15

G84717
actin depolymerizing factor 6 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C;Accession: G84717
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eissen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: G84717
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-132 <STO>
A;Cross-references: GB:AE002093; NID:94432815; PIDN:AAD20665.1; GSPDB:GN00139

C;Genetics:
A;Gene: At2g31200
A;Map position: 2
C;Superfamily: cofilin

Alignment Scores:

Pred. No.:	2.29e-10	Length:	132
Score:	208.00	Matches:	41
Percent Similarity:	63.48%	Conservative:	32

Best Local Similarity: 35.65% Mismatches: 32
 Query Match: 23.09% Indels: 10
 DB: 2 Gaps: 3

US-10-649-952A-2 (1-501) x G84717 (1-132)

```

QY 88 AAGAGCGCAAGAGCGGTCTCTCTGCTGAGTGAGGACAGAGACATCATCCTG 147
    |||||  ::  |||::|  ::  |||  |||||  ::|::|  ::|::|  ::|::|
Db 17 LysLysThrHisArgTyrValPheLysLeuLysLysLysGluValValVal 36
    |||::|  |||::|  |||::|  |||::|  |||::|  |||::|  |||::|  |||::|
QY 148 GAGGAGGCAAGGAGATCCTGTGGCGCATGTGGCCAGACTGTCGACGATCCCTAGCC 207
    |||::|  |||::|  |||::|  |||::|  |||::|  |||::|  |||::|  |||::|
Db 37 GluLys-----ThrGlyAsnProThrGluSerTyrAspAsp----- 48
    |||::|  |||::|  |||::|  |||::|  |||::|  |||::|  |||::|  |||::|
QY 208 ACCTTTGTCAAGATGTCAGATAAGACTGCCGTATGCCCTCTATGCAACCTAT 267
    |||::|  |||::|  |||::|  |||::|  |||::|  |||::|  |||::|  |||::|
Db 49 ---PheLeuAlaSerLeuProAspAsnAspCysArgTyrAlaValTyrAspPhe 67
    |||::|  |||::|  |||::|  |||::|  |||::|  |||::|  |||::|  |||::|
QY 268 GAGACCAAGGAGAGCAAGAGGAGGATCTGCTGTTTATCTTC---TGGGCCCGGAGTCT 324
    |||  |||::|  |||::|  |||::|  |||::|  |||::|  |||::|  |||::|
Db 68 valThrSerGluAsnCysGlnLysSerLysLysPhePheAlaTrpSerProSerThr 87
    |||  |||::|  |||::|  |||::|  |||::|  |||::|  |||::|  |||::|
QY 325 GCGCCCTTAAGAGCAAAATGATTATGCCAGCTCCAAGGACGCCATCAAGAGAGAGCTG 384
    |||  |||::|  |||::|  |||::|  |||::|  |||::|  |||::|  |||::|
Db 88 SerGlyIleArgAlaLysValLeuTyrSerThrSerLysAspGlnLeuSerArgGluLeu 107
    |||  |||::|  |||::|  |||::|  |||::|  |||::|  |||::|  |||::|
QY 385 ACAGGGATCAAGCATGAATTGCAAGCAAACTGCTACGAGGAGTC 429
    |||  |||::|  |||::|  |||::|  |||::|  |||::|  |||::|  |||::|
Db 108 GlnGlyIleHisTyrGluIleGlnAlaThrAspProThrGluVal 122
    |||  |||::|  |||::|  |||::|  |||::|  |||::|  |||::|  |||::|
  
```

Search completed: May 13, 2005, 10:00:35
 Job time : 36.5 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: May 13, 2005, 09:46:55 ; Search time 137 Seconds
(without alignments)
3745.280 Million cell updates/sec

Title: US-10-649-952A-2

Perfect score: 901

Sequence: 1 atggctccggtgtgctgt.....tggagggaagcctttgtga 501

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p,model -DEV=xlp
-Q/cgr2_1/USPTO_spool_p/US10649952/runat 13052005_102649_27313/app_query.fasta_1.647
-DB-Uniprot -Qfmt=fastan -SUFFIX=n2p.rup -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdd -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10649952 @CGN 1.1 244 @runat 13052005_102649_27313 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -JONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt 03.*

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	841	93.3	165	1 COPI_HUMAN	P23528 homo sapien
2	837	92.9	165	1 COPI_RAT	P45592 rattus norv
3	836	92.8	165	1 COPI_PIG	P10668 sus scrofa
4	836	92.8	165	1 COPI_SHEEP	O6b7m7 ovis aries
5	834	92.6	165	1 COPI_MOUSE	P18760 mus musculus
6	831	92.2	229	2 COFC22	Q9CX22 mus musculus
7	709	78.7	166	1 COFI_CHICK	P15666 gallus gall
8	702	77.9	166	1 COF2_MOUSE	P45591 xenopus lae
9	699	77.6	166	1 COF2_MOUSE	P45591 xenopus lae
10	693	76.9	166	2 O6N2W3	Q9Y281 homo sapien
11	659	73.1	168	2 O6N2W3	O6N2W3 brachydanio
12	656	72.8	168	1 COF2_XENLA	O6N2W3 xenopus tro
13	649	72.0	168	1 COF2_XENLA	P45593 xenopus lae
14	625.5	69.4	165	2 O6TH32	O6TH32 brachydanio
15	615.5	68.3	164	1 DEST_CHICK	P18359 gallus gall
16	606.5	67.3	164	1 DEST_MOUSE	Q9R0P5 mus musculus

17	604.5	67.1	165	2	Q6DV06	Q6dv06 gekko japon
18	601.5	66.8	164	1	DEST_HUMAN	P60981 homo sapien
19	601.5	66.8	164	1	DEST_PIG	P60982 sus scrofa
20	598.5	66.4	164	2	Q7M0E3	Q7m0e3 rattus norv
21	392.5	43.6	163	2	Q7ZWD8	Q7zwd8 brachydanio
22	368.5	40.9	111	2	O8N1B5	O8n1b5 homo sapien
23	310.5	34.5	153	2	Q7ZXD4	Q7zxd4 xenopus lae
24	282.5	31.4	153	2	Q6C0Y0	Q6c0y0 yarrowia li
25	280	31.1	143	2	Q9HF97	Q9hf97 zygosacchar
26	276	30.6	143	2	Q6BWX4	Q6bwx4 debaryomyce
27	273	30.3	143	2	Q6CQ22	Q6cq22 kluyveromyce
28	271	30.1	143	2	Q7S9P0	Q7s9p0 ashbya goss
29	268	29.7	143	2	Q96VU9	Q96vu9 pichia angu
30	267.5	29.7	143	1	COFI_YEAST	Q03048 saccharomyc
31	265	29.4	143	2	Q6FV81	Q6fv81 candida gla
32	257.5	28.6	156	2	Q05307	Q05307 saccharomyc
33	257	28.5	137	1	ACTP_ACACA	P31567 acanthamoeb
34	254	28.2	137	1	COFI_SCHPO	P78929 schizosacch
35	230	25.5	137	1	COFI_DICDI	P54706 dictyostell
36	227.5	25.2	139	2	Q6T8D2	Q6t8d2 helianthus
37	227	25.2	139	1	ADF3_MAIZE	Q41764 zea mays (m
38	224.5	24.9	146	2	O8LCM6	Q8lcm6 arabidopsis
39	222.5	24.7	463	2	O6JAG0	O6jag0 sorghum bic
40	220.5	24.5	139	1	ADF1_PETHY	Q9fvi2 petunia hyb
41	220	24.4	140	2	Q9M594	Q9m594 elaeis guin
42	219.5	24.4	139	1	ADF1_ARATH	Q39250 arabidopsis
43	219.5	24.4	143	1	ADF2_PETHY	Q9fvi1 petunia hyb
44	217.5	24.1	139	1	ADF4_ARATH	Q9zak3 arabidopsis
45	216	24.0	139	2	Q84TE3	Q84tb3 cryza sativ

ALIGNMENTS

RESULT 1

COFI_HUMAN	STANDARD;	PRT;	165 AA.
ID	COFI_HUMAN		
AC	P23528; Q9UCA2;		
DT	01-NOV-1991 (Rel. 20, Created)		
DT	25-JAN-2005 (Rel. 46, Last sequence update)		
DT	25-JAN-2005 (Rel. 46, Last annotation update)		
DE	Cofilin, non-muscle isoform (Cofilin-1) (18 kDa phosphoprotein) (p18).		
GN	Name=COF1; Synonyms=CF1;		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Placenta;		
RX	MEDLINE=91088330; PubMed=2263493;		
RA	Ogawa K., Tashima M., Yumoto Y., Okuda T., Sawada H., Okuma M.,		
RA	Mariyama Y.;		
RT	"Coding sequence of human placenta cofilin cDNA.";		
RL	Nucleic Acids Res. 18:7169-7169(1990).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RA	der Steege G., Draaijers T.G., Grootsholten P.M., Ozinga J.,		
RA	Anzevino R., Velona I., Brahe C., Scheffer H., van Ommen G.J.B.,		
RA	Buys C.H.C.M.;		
RN	[3]		
RP	Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.		
RN	[4]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=96393653; PubMed=8800436;		
RA	Gillett G.T., Fox M.F., Rowe P.S.N., Casimir C.M., Povey S.;		
RT	"Mapping of human non-muscle type cofilin (COF1) to chromosome 11q13		
RT	and muscle type cofilin (COF2) to chromosome 14.";		
RL	Ann. Hum. Genet. 60:201-211(1996).		
RN	[4]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Lung, Ovary, Placenta, and Uterus;		
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;		
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,		

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., Morley P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Woley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fabey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.J., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [5]
RP SEQUENCE OF 1-20.
RC TISSUE=Platelet;
RX MEDLINE=22608298; PubMed=12665801; DOI=10.1038/nbt810;
RA Gevaert K., Goethals M., Martens L., Van Damme J., Staes A.,
RA Thomas G.R., Vandekerckhove J.;
RT "Exploring proteomes and analyzing protein processing by mass
spectrometric identification of sorted N-terminal peptides.";
RL Nat. Biotechnol. 21:566-569 (2003).
RN [6]
RP SEQUENCE OF 51-70.
RC TISSUE=Platelet;
RX MEDLINE=94311852; PubMed=8037689;
RA Davidson M.M., Haslam R.J.;
RT "Dephosphorylation of cofilin in stimulated platelets: roles for a
GTP-binding protein and C22";
RL Biochem. J. 301:41-47 (1994).
CC -1- FUNCTION: Controls reversibly actin polymerization and
depolymerization in a pH-sensitive manner. It has the ability to
bind G- and F-actin in a 1:1 ratio of cofilin to actin. It is the
major component of intranuclear and cytoplasmic actin rods.
CC -1- SUBCELLULAR LOCATION: Intranuclear and cytoplasmic; almost
completely in nucleus in cells exposed to heat shock or 10%
dimethyl sulfoxide.
CC -1- TISSUE SPECIFICITY: Widely distributed in various tissues.
CC -1- PTM: The phosphorylation of Ser-23 may prevent recognition of the
nuclear localization signal.
CC -1- SIMILARITY: Belongs to the actin-binding proteins ADF family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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or send an email to license@isb-sib.ch).
CC
CC EMBL; D00682; BAA00589.1; -
CC EMBL; U21909; ARA64501.1; -
CC EMBL; X95404; CAA64685.1; -
CC EMBL; BC011005; AAH11005.1; -
CC EMBL; BC012265; AAH12265.1; -
CC EMBL; BC012318; AAH12318.1; -
CC EMBL; BC018256; AAH18256.1; -
CC PIR; S12632; S12632.
CC HSSP; P18282; IAK6.
CC SWISS-2DPAGE; P23528; HUMAN.
CC Aarhus/Ghent-2DPAGE; 4; IEF.
CC OGP; P23528; -
CC Genew; HGNC:1874; CFL1.
CC H-InVDB; HIX0009808; -
CC MIM; 601442; -
CC GO; GO:0005634; C:nucleus; TAS.
CC GO; GO:0030036; P:actin cytoskeleton organization and biogenesis; TAS.
CC GO; GO:0007266; P:Rho protein signal transduction; TAS.

DR InterPro; IPR002108; Actbind_cofln.
DR Pfam; PF00241; Cofilin_ADF; 1.
DR PRINTS; PR00006; COFILIN.
DR ProDom; PD002129; Actbind_cofln; 1.
DR SMART; SM00102; ADF; 1.
DR PROSITE; PS00345; ACTIN DEPOLYMERIZING; 1.
KW Actin-binding; Cytoskeleton; Direct protein sequencing;
KW Nuclear protein; Phosphorylation.
FT INIT MET 29 0
FT DOMAIN 29 33 Nuclear localization signal (Potential).
FT DOMAIN 105 124 Actin-binding (Potential).
FT MOD_RES 23 23 Phosphoserine (Probable).
SQ SEQUENCE 165 AA; 18371 MW; EC9251A6D1C7C84C CRC64;

Alignment Scores:
Pred. No.: 2 38e-64 Length: 165
Score: 841.00 Matches: 165
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 93.34% Indels: 0
DB: 1 Gaps: 0

US-10-649-952a-2 (1-501) x COFI_HUMAN (1-165)

QY 4 GCCTCCGGTGTGGCTGTCTCTGATGTGCATCAAGGTGTTCACGACATGAAGTCCGT 63
DB 1 AlaSerGlyValAlaValSerAspGlyValIleLysValPheAsnAspMetLysValArg 20

QY 64 AGTCTTCAAGCCGAGAGGAGGTGAAGACGCGAAGAGCGGTGCTCTTCTGCTCAGT 123
DB 21 LysSerSerThrProGluGluValLysLysArgLysLysAlaValLeuPheCysLeuSer 40

QY 124 GAGCACAAGAAAGAACATCATCTCGAGGAGGCGAAGAGAGATCTGTGGCGGATGTGGGC 183
DB 41 GluAspLysLysAsnIleIleLeuGluGluLysGluLeuValGlyAspValGly 60

QY 184 CAGACTGTTCGACGATCCCTACGCCACCTTTGTCAAGATGTGCCAGATAAGGACTGCCGC 243
DB 61 GluThrValAspAspProTyrAlaThrPheValLysMetLeuProAspLysAspCysArg 80

QY 244 TATGCCCTCTATGATGCAACCTATGAGACCAAGAGAGCAAGAGGAGATCTGGTGT 303
DB 81 TyrAlaLeuTyrAspAlaThrTyrGluThrLysGluSerLysLysGluAspLeuValPhe 100

QY 304 ATCTTCTGGCCCCCGAGTCTGCGCCCTTAAGAGCAAAATGATTATGCAGCTCCAAG 363
DB 101 IlePheThrAlaProGluSerAlaProLeuLysSerLysMetIleTyrAlaSerSerLys 120

QY 364 GAGCCATCAAGAAAGAGCTGACAGGGATCAAGCATGAATTGCAAGCAAACTGCTACGAG 423
DB 121 AspAlaIleLysLysLysLeuThrGlyIleLysHisGluLeuGlnAlaAsnCysTyrGlu 140

QY 424 GAGGTCAAGACCGCTGCACCTTGGCAGAGAGCAAGCTGGGGGGGAGTGGGGTCACTCCCTG 483
DB 141 GluValLysAspArgCysThrLeuAlaGluLysLeuGlySerAlaValIleSerLeu 160

QY 484 GAGGGCAAGCCTTTG 498
DB 161 GluGlyLysProLeu 165

RESULT 2
COFI_RAT
ID COFI_RAT STANDARD; PRT; 165 AA.
AC P45592;
DT 01-NOV-1995 (Rel. 32, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Cofilin, non-muscle isoform (Cofilin-1).
GN NamesCfl1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;


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RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=Wistar; TISSUE=Brain;
RL  Shiraawa T., Takahashi H., Sakamoto K., Kawashima A., Akashi T.;
RA  Submitted (OCT-1991) to the EMBL/GenBank/DBJ databases.
RL  [2]
RP  SEQUENCE, ACETYLATION, PHOSPHORYLATION SITE SER-23, AND MASS
RP  SPECTROMETRY.
RC  TISSUE=Parotid gland;
RA  Kanamori T., Suzuki M.M., Titani K.;
RT  "Complete amino acid sequences and phosphorylation sites, determined
RT  by Edman degradation and mass spectrometry, of rat parotid destrin-and
RT  cofillin-like protein.";
RL  Submitted (AUG-1998) to the PIR data bank.
CC  -1- FUNCTION: Controls reversibly actin polymerization and
CC  depolymerization in a pH-sensitive manner. It has the ability to
CC  bind G- and F-actin in a 1:1 ratio of cofillin to actin. It is the
CC  major component of intranuclear and cytoplasmic actin rods (By
CC  similarity).
CC  -1- SUBCELLULAR LOCATION: Intranuclear and cytoplasmic (By
CC  similarity).
CC  -1- TISSUE SPECIFICITY: Widely distributed in various tissues (By
CC  similarity).
CC  -1- PTM: The phosphorylation of Ser-23 may prevent recognition of the
CC  nuclear localization signal.
CC  -1- SIMILARITY: Belongs to the actin-binding proteins ADF family.
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CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
-----
DR  EMBL; X62908; CAA44694.1; -.
DR  FRL; S49101; S49101.
DR  HSP; P18282; IAK6.
DR  RGD; 69285; Cfil.
DR  InterPro; IPR002108; Actbind_coflin.
DR  Pfam; PF00241; Cofilin_ADF; 1.
DR  PRINTS; PR00006; COFILIN.
DR  ProDom; PD002129; Actbind_coflin; 1.
DR  SMART; SM00102; ADF; 1.
DR  PROSITE; PS00325; ACTIN DEPOLYMERIZING; 1.
KW  Acetylation; Actin-binding; Cytoskeleton; Direct protein sequencing;
KW  Nuclear protein; Phosphorylation.
FT  INIT_MET . 0
FT  MOD_RES . 1 1 N-acetylalanine.
FT  DOMAIN 29 33 Nuclear localization signal (Potential).
FT  DOMAIN 105 124 Actin-binding (Potential).
FT  MOD_RES 23 23 Phosphoserine.
SQ  SEQUENCE 165 AA; 18401 MW; AD8FFACB671CA5E7 CRC64;

Alignment Scores:
Pred. No.: 5,29e-64 Length: 165
Score: 837.00 Matches: 164
Percent Similarity: 99.39% Conservative: 0
Best Local Similarity: 99.39% Mismatches: 1
Query Match: 92.90% Indels: 0
DB: 1 Gaps: 0

US-10-649-952a-2 (1-501) x COFI_RAT (1-165)

QY 4 GCCTCCGGTGGCTGCTCTGATGGTGTTCATCAAGGTGTTCAACGACATGAAGTGGCT 63
DB 1 AlaSerGlyValAlaValSerAspGlyValIleLysValPheAsnAspMetLysValArg 20
QY 64 AAGTCTTCAACGCCAGAGGAGGTGAAGAAGCGAAGGCGGTCTCTTCTGCTGAGT 123
DB 21 LysSerSerThrProGluGluValLysLysArgLysLysAlaValLeuPheCysLeuSer 40
QY 124 GAGGACAAGAAGAACATCATCTCTGGAGGAGGAGGAGATCCTGTGGTGGCGATGTGGGC 183

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Db 41 GluAspLysLysAsnIleIleLeuGluGluGlyLysGluIleLeuValGlyAspValGly 60
QY 184 CAGACTGTCTGACGATCCCTACGCCACCTTTGTCAAGATGCTGCAGATAAGGACTGCCGC 243
Db 61 GluThrValAspAspProTyrThrThrPheValLysMetLeuProAspLysAspCysArg 80
QY 244 TATGCCCTCTATGATGCAACCTATGAGACCAAGAGAGAGCAAGAGGAGATCTGGTGT 303
Db 81 TyrAlaLeuTyrAspAlaThrTyrGluThrLysGluSerLysLysGluAspLeuValPhe 100
QY 304 ATCTTCTGGCCCGCCGAGCTGCGCCCTTAAGAGCAAAATGATTTATGCAGCTCCAA 363
Db 101 IlePheTrpAlaProGluSerAlaProLeuLysSerLysMetIleTyrAlaSerSerLys 120
QY 364 GAGCCATCAAGAAGAGCTGACAGGATCAAGCATCAATTCGAAGCAAACTGCTACGAG 423
Db 121 AspAlaIleLysLysLysLeuThrGlyIleLysHisGluLeuGlnAlaAsnCysTyrGlu 140
QY 424 GAGGTCAAGGACCGCTGACCCCTGGCAGAGAACTGGGGGCGAGTGGCGTCACTCCCTG 483
Db 141 GluValLysAspArgCysThrLeuAlaGluLysLeuGlyGlySerAlaValIleSerLeu 160
QY 484 GAGGGCAAGCCCTTTG 498
Db 161 GluGlyLysProLeu 165

RESULT 3
COFI_PIG STANDARD; PRT; 165 AA.
AC P10668; Q29374;
DT 01-JUL-1989 (Rel. 11, Created)
DT 25-JAN-2005 (Rel. 46, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Cofilin, non-muscle isoform (Cofilin-1).
GN Names:CFIL1;
OS Sus scrofa (Pig).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=88298817; PubMed=3403546;
RA Matsuzaki F., Matsumoto S., Yahara I., Yonezawa N., Nishida E.,
RA Sakai H.;
RT "Cloning and characterization of porcine brain cofilin cDNA. Cofilin
RT contains the nuclear transport signal sequence.";
RL J. Biol. Chem. 263:11564-11568(1988).
RN [2]
RP SEQUENCE OF 1-103 FROM N.A.
RC TISSUE=Small intestine;
RX MEDLINE=96327607; PubMed=8672129;
RA Winteroe A.K., Fredholm M., Davies W.;
RT "Evaluation and characterization of a porcine small intestine cDNA
RT library: analysis of 839 clones.";
RL Mamm. Genome 7:509-517(1996).
CC -1- FUNCTION: Controls reversibly actin polymerization and
CC depolymerization in a pH-sensitive manner. It has the ability to
CC bind G- and F-actin in a 1:1 ratio of cofilin to actin. It is the
CC major component of intranuclear and cytoplasmic actin rods.
CC -1- SUBCELLULAR LOCATION: Intranuclear and cytoplasmic; almost
CC completely in nucleus in cells exposed to heat shock or 10%
CC dimethyl sulfoxide.
CC -1- TISSUE SPECIFICITY: Widely distributed in various tissues.
CC -1- PTM: The phosphorylation of Ser-23 may prevent recognition of the
CC nuclear localization signal.
CC -1- MISCELLANEOUS: A double mutation of Lys-111 and Lys-113 to Gln
CC produces a mutant with no ability to depolymerize or bind F-actin.
CC -1- SIMILARITY: Belongs to the actin-binding proteins ADF family.
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DR EMBL; M20866; AAA31020.1; -;
DR PIR; A29240; A29240.
DR HSPF; F18282; 1AK6.
DR InterPro; IPR002108; Actbind_coflin.
DR Pfam; PF00241; Cofilin_ADF; 1.
DR PRINTS; PR00006; COFILIN.
DR ProDom; PD002129; Actbind_coflin; 1.
DR SMART; SM00102; ADF; 1.
DR PROSITE; PS00325; ACTIN_DEPOLYMERIZING; 1.
KW Actin-binding; Cytoskeleton; Direct protein sequencing;
KW Nuclear protein; Phosphorylation.
FT INIT MET 0 By similarity.
FT DOMAIN 29 33 Nuclear localization signal (Potential).
FT DOMAIN 105 124 Actin-binding (Potential).
FT MOD_RES 23 23 Phosphoserine (By similarity).
FT MUTAGEN 111 111 K->Q: Slight modification of activity.
FT MUTAGEN 113 113 K->Q: Impairs interaction with actin.
SQ SEQUENCE 165 AA; 18387 MW; EC9241B6D1D7D84C CRC64;

Alignment Scores:
Pred. No.: 6.46e-64 Length: 165
Score: 836.00 Matches: 164
Percent Similarity: 99.39% Conservative: 0
Best Local Similarity: 99.39% Mismatches: 1
Query Match: 92.79% Indels: 0
DB: 1 Gaps: 0

US-10-649-952A-2 (1-501) x COFI_PIG (1-165)

Qy 4 GCCTCCGGTGGGTCTCTGATGTTTCATCAAGGTGTTCAACGACATGAAGTGGT 63
Db 1 AlaserGlyValAlaValSerAspGlyValIleLysValPheAsnAspMetLysValArg 20
Qy 64 AAGTCTTCAACGCCAGGAGGTGAAGAGCGGCGGTCTCTTCTGCTCGT 123
Db 21 LysSerSerThrProGluValLysArgLysLysAlaValLeuPheCysLeuSer 40
Qy 124 GAGCAAGACATCATCTCGAGGCGGAGGATCTCTGGTGGCGATGTGGGC 183
Db 41 GluAspLysLysAsnIleLeuGluGluGlyLysGluIleLeuValGlyAspValGly 60
Qy 184 CAGACTGTGCGACGATCCCTACGCCACCTTCTCAAGATGCTGCCAGATAAGGACTGCCGC 243
Db 61 GlnThrValAspProTyrAlaThrPheValLysMetLeuProAspLysAspCysArg 80
Qy 244 TATGCCCTCTATGATCAACCTATGACACCAAGGAGGAGGAGGATCTCGTGT 303
Db 81 TyrAlaLeuTyrAspAlaThrTyrGluThrLysGluSerLysLysGluAspLeuValPhe 100
Qy 304 ATCTTCTGGGCCCCGAGCTCGCCCTTAAAGAGCAAAATGATTTATGCCAGCTCCAG 363
Db 101 IlePheTrpAlaProGluCysAlaProLeuLysSerLysMetIleTyrAlaSerSerLys 120
Qy 364 GACGCCATCAAGAAGAGCTCAGAGGATCAAGATGAATTTGCAAGCAAACTGTACGAG 423
Db 121 AspalalleLysLysLeuThrGlyLysLysGluLeuGlnAlaAsnLysCysTyrGlu 140
Qy 424 GAGGTCAAGGACCGCTGCACCTCGCAGAGAGCTGGGGGCGAGTGGCGTTCATCTCCCTG 483
Db 141 GluValLysAspArgCysThrLeuAlaGluLysLeuGlyGlySerAlaValIleSerLeu 160
Qy 484 GAGGCAAGCCTTTG 498
Db 161 GluGlyLysProLeu 165

RESULT 4

COFI_SHEEP
ID _COFI_SHEEP STANDARD; PRT; 165 AA.
AC Q6B7M7; 2004 (Rel. 45, Created)
DT 25-OCT-2005 (Rel. 46, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DB Cofilin, non-muscle isoform (Cofilin-1).
GN Name=CFIL1; (Sheep).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Endometrium;
RA Welker J.E., Ott T.L.;
RT "Cloning and characterization of cofilin-1 expression in cyclic and
RT early pregnant ovine endometrium following isolation by yeast-two
RT hybrid screening";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Controls reversibly actin polymerization and
CC depolymerization in a pH-sensitive manner. It has the ability to
CC bind G- and F-actin in a 1:1 ratio of cofilin to actin. It is the
CC major component of intranuclear and cytoplasmic actin rods (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Intranuclear and cytoplasmic (By
CC similarity).
CC -!- PTM: The phosphorylation of Ser-23 may prevent recognition of the
CC nuclear localization signal (By similarity).
CC -!- SIMILARITY: Belongs to the actin-binding proteins ADF family.

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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC EMBL; AY676116; AAT77679.1; -;
DR ProDom; PD002129; Actbind_coflin; 1.
DR PROSITE; PS00325; ACTIN_DEPOLYMERIZING; 1.
KW Actin-binding; Cytoskeleton; Nuclear protein; Phosphorylation.
FT INIT_MET 0 By similarity.
FT DOMAIN 29 33 Nuclear localization signal (Potential).
FT DOMAIN 105 124 Actin-binding (Potential).
FT MOD_RES 23 23 Phosphoserine (By similarity).
SQ SEQUENCE 165 AA; 18387 MW; EC9241B6D1D7D84C CRC64;
Alignment Scores:
Pred. No.: 6.46e-64 Length: 165
Score: 836.00 Matches: 164
Percent Similarity: 99.39% Conservative: 0
Best Local Similarity: 99.39% Mismatches: 1
Query Match: 92.79% Indels: 0
DB: 1 Gaps: 0
US-10-649-952A-2 (1-501) x COFI_SHEEP (1-165)
Qy 4 GCCTCCGGTGGGTCTCTGATGTTTCATCAAGGTGTTCAACGACATGAAGTGGT 63
Db 1 AlaserGlyValAlaValSerAspGlyValIleLysValPheAsnAspMetLysValArg 20
Qy 64 AAGTCTTCAACGCCAGGAGGTGAAGAGCGGCGGTCTCTTCTGCTCGT 123
Db 21 LysSerSerThrProGluValLysArgLysLysAlaValLeuPheCysLeuSer 40
Qy 124 GAGCAAGACATCATCTCGAGGCGGAGGATCTCTGGTGGCGATGTGGGC 183
Db 41 GluAspLysLysAsnIleLeuGluGluGlyLysGluIleLeuValGlyAspValGly 60
Qy 184 CAGACTGTGCGACGATCCCTACGCCACCTTCTCAAGATGCTGCCAGATAAGGACTGCCGC 243
Db 61 GlnThrValAspProTyrAlaThrPheValLysMetLeuProAspLysAspCysArg 80
Qy 244 TATGCCCTCTATGATCAACCTATGACACCAAGGAGGAGGAGGATCTCGTGT 303
Db 81 TyrAlaLeuTyrAspAlaThrTyrGluThrLysGluSerLysLysGluAspLeuValPhe 100
Qy 304 ATCTTCTGGGCCCCGAGCTCGCCCTTAAAGAGCAAAATGATTTATGCCAGCTCCAG 363
Db 101 IlePheTrpAlaProGluCysAlaProLeuLysSerLysMetIleTyrAlaSerSerLys 120
Qy 364 GACGCCATCAAGAAGAGCTCAGAGGATCAAGATGAATTTGCAAGCAAACTGTACGAG 423
Db 121 AspalalleLysLysLeuThrGlyLysLysGluLeuGlnAlaAsnLysCysTyrGlu 140
Qy 424 GAGGTCAAGGACCGCTGCACCTCGCAGAGAGCTGGGGGCGAGTGGCGTTCATCTCCCTG 483
Db 141 GluValLysAspArgCysThrLeuAlaGluLysLeuGlyGlySerAlaValIleSerLeu 160
Qy 484 GAGGCAAGCCTTTG 498
Db 161 GluGlyLysProLeu 165
RESULT 4

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RL and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: Controls reversibly actin polymerization and
 CC depolymerization in a pH-sensitive manner. It has the ability to
 CC bind G- and F-actin in a 1:1 ratio of cofillin to actin. It is the
 CC major component of intranuclear and cytoplasmic actin rods.
 CC -!- SUBCELLULAR LOCATION: Intranuclear and cytoplasmic.
 CC -!- TISSUE SPECIFICITY: Predominantly expressed in skeletal muscle.
 CC -!- PTM: The phosphorylation of Ser-24 may prevent recognition of the
 CC nuclear localization signal.
 CC -!- SIMILARITY: Belongs to the actin-binding proteins ADF family.
 CC -----
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 CC -----
 CC EMBL; L29468; AAA37433.1; --
 CC EMBL; BC007138; AAH07138.1; --
 CC PIR; A53812; A53812.
 CC HSP; P18282; IAK6.
 CC MGD; MG1:101763; CF12.
 CC InterPro; IPR002108; Actbind_coflin.
 CC Pfam; PF00241; Cofilin_ADF; 1.
 CC PRINTS; PR00006; COFILIN.
 CC ProDom; PD002129; Actbind_coflin; 1.
 CC SMART; SM00102; ADF; 1.
 CC PROSITE; PS00325; ACTIN DEPOLYMERIZING; 1.
 CC Actin-binding; Cytoskeleton; Nuclear localization signal (Potential).
 FT DOMAIN 30 34
 FT DOWAIN 106 125 Actin-binding (Potential).
 FT MOD RES 24 24 Phosphoserine (By similarity).
 SQ SEQUENCE 166 AA; 18709 MW; 486D7E5AE9FE1CC CRC64;
 Alignment Scores:
 Pred. No.: 2,76e-52 Length: 166
 Score: 702.00 Matches: 135
 Percent Similarity: 89.76% Conservative: 14
 Best Local Similarity: 81.33% Mismatches: 17
 Query Match: 77.91% Indels: 0
 DB: 1 Gaps: 0
 US-10-649-952A-2 (1-501) x COF2_MOUSE (1-166)
 Qy 1 ATGGCTCCGGTGGCTGCTCTGATGGTGTCTCAAGGTTTCACGACATGAAGTG 60
 Db 1 MetAlaSerGlyValThrValAsnAspGluValIleLysValPheAsnAspMetLysVal 20
 Qy 61 CGTAAGTCTTCAACGCCAGGAGGTGTAGAGCGCAGAGCGGCTCTTCTGCGCTG 120
 Db 21 ArgLysSerSerThrGlnGluGluIleLysLysArgLysLysAlaValLeuPheCysLeu 40
 Qy 121 AGTGAGGACAGAAAGACATCATCTGCGAGAGGCGGAGAGATCTCTGGTGGCGATGTG 180
 Db 41 SerAspAspLysArgGlnIleValGluGluAlaLysGlnIleValGlyAspIle 60
 Qy 181 GCGCAGACTGTGAGGATCCCTACGCCACCTTGTCAAGATGCTGCCAGATAAGGATGCG 240
 Db 61 GlyAspThrValGluAspProTyrThrSerPheValLysLeuLeuProLeuAsnAspCys 80
 Qy 241 CGCTATGCTCTATGACCACTATCAGACCAAGGAGGAGGAGGAGGATCTGGTG 300
 Db 81 ArgTyrAlaLeuTyrAspAlaThrTyrGluThrLysGluSerLysGluAspLeuVal 100
 Qy 301 TTTATCTTCTGGGCCCCGAGTCTGCGCCCTTAAAGAGCAAAATGATTATGCGAGCTCC 360

Db 101 PheilePheTrpAlaProGluSerAlaProLeuLysSerLysMetIleTyrAlaSerSer 120
 Qy 361 AAGGACCCCATCAGAGAGAGCTGACAGGATCATGAGCATGATGCGAAGCAATGCTGCTAC 420
 Db 121 LysAspAlaIleLysLysLysPheThrGlyIleLysHisGluTrpGlnValAsnGlyLeu 140
 Qy 421 GAGGAGGTGACAGGACCCCTGACCTGCGACAGAGAGCTGGGGGCGACGTGCGGTCTATCTCC 480
 Db 141 AspAspIleLysAspArgSerThrLeuGlyLysLeuGlyLysValValValSer 160
 Qy 481 CTGGAGGCGCAAGCTTTG 498
 Db 161 LeuGluGlyLysProLeu 166
 RESULT 9
 COF2 HUMAN STANDARD; PRT; 166 AA.
 ID COF2 HUMAN AC Q9Y281;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Cofilin, muscle isoform (Cofilin-2).
 GN Name=COF2;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Jin J., Li G., Hu S., Li W., Yuan J., Qiang B.;
 RT "Isolation of two isoforms of human cofilin cDNA";
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=21315834; PubMed=11422377;
 RA Thirion C., Stucka R., Mendel B., Gruhler A., Jaksch M., Nowak K.J.,
 RA Binz N., Laing N.G., Lockmuller H.;
 RT "Characterization of human muscle type cofilin (CFL2) in normal and
 RT regenerating muscle";
 RL Eur. J. Biochem. 268:3473-3482(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RT TISSUE=Bone marrow, Placenta, and Skeletal muscle;
 RX MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Pahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.J., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: Controls reversibly actin polymerization and
 CC depolymerization in a pH-sensitive manner. It has the ability to
 CC bind G- and F-actin in a 1:1 ratio of cofillin to actin. It is the
 CC major component of intranuclear and cytoplasmic actin rods (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Intranuclear and cytoplasmic (By
 CC similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;

CC Comment-Isoforms are identical at the level of the protein
sequence;
CC Names=CFL2b;
CC IsoId=Q9Y281-1; Sequence=Displayed;
CC Names=CFL2a;
CC IsoId=Q9Y281-2; Sequence=Not described;
CC -1- TISSUE SPECIFICITY: Isoform CFL2b is expressed predominantly in
skeletal muscle and heart, while isoform CFL2a is expressed in
various tissues.
CC -1- PTM: The phosphorylation of Ser-24 may prevent recognition of the
nuclear localization signal.
CC -1- SIMILARITY: Belongs to the actin-binding proteins ADF family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

CC EMBL; AF134802; AAD31280.1; -
CC EMBL; AF134803; AAD31281.1; -
CC EMBL; AF283513; AAF97934.1; -
CC EMBL; AF242299; AAF64498.1; -
CC EMBL; BC011444; AAH11444.1; -
CC EMBL; BC022364; AAH22364.1; -
CC EMBL; BC022876; AAH22876.1; -
CC HSP; P18282; IAK6.
CC Genew; HGNC:1875; CFL2.
CC MIM; 601443; -
CC InterPro; IPR002108; Actbind_cofln.
CC Pfam; PF00241; Cofilin_ADF; 1.
CC PRINTS; PR00006; COFILIN.
CC SMART; PD002129; Actbind_cofln; 1.
CC PROSITE; PS00325; ACTIN_DEPOLYMERIZING; 1.
CC Actin-binding; Alternative splicing; Cytoskeleton; Nuclear protein;
KW Phosphorylation.
FT DOMAIN 30 34 Nuclear localization signal (Potential).
FT DOMAIN 106 125 Actin-binding (Potential).
FT MOD_RES 24 24 Phosphoserine (by similarity).
SQ SEQUENCE .166 AA; 18736 MW; 48B6DCCAE9FE1CC CRC64;

Alignment Scores:
Pred. No.: 5.03e-52 Length: 166
Score: 699.00 Matches: 134
Percent Similarity: 89.76% Conservative: 15
Best Local Similarity: 80.72% Mismatches: 17
Query Match: 77.58% Indels: 0
DB: 1 Gaps: 0

US-10-649-952A-2 (1-501) x COP2_HUMAN (1-166)

QY 1 ATGGCTCCGGTGGCTGCTCTGATGCTCATCAAGGTGTCAACGACATGAAGGTG 60
Db 1 MetAlaSerGlyValThrValAsnAspGluValIleLysValPheAsnAspMetLysVal 20

QY 61 CGTAAGCTTCAACGCGAGGAGGTGAGAACGCGAAGCGGTGCTCTCTGCTG 120
Db 21 ArgLysSerSerThrGlnGluIleLysLysArgLysLysAlaValLeuPheCysLeu 40

QY 121 AGTGAGACAAAGAACAATCATCTCGAGGAGGCAAGAGATCTGTGGGCGATGTG 180
Db 41 SerAspAspLysArgGlnIleIleValGluGluAlaLysGlnIleLeuValGlyAspIle 60

QY 181 GGCGACAGTGTGACGATCCCTACGCCACCTTTGTCAAGATGCTGCCAGATGAAGGACTGC 240
Db 61 GlyAspThrValGluAspProTyThrSerPheValLysLeuLeuProLeuAsnAspCys 80

QY 241 CGCTATGCTCTATGATGCAACTATGAGACCAAGAGAGCAAGAGGATCTGGTG 300
Db 81 ArgTyAlaLeuTyArgAlaThrTyThrGluThrLysGluSerLysLysGluAspLeuVal 100

QY 301 TTATATCTTTGGCCCCCGAGTCTGGCCCTTAAGAGCAAAATGATTTATGCAGCTCC 360
Db 101 PheIlePheTrpAlaProGluSerAlaProLeuLysSerLysMetIleTyAlaSerSer 120

QY 361 AAGGAGCCATCAAGAAGAGCTGACAGGATCAAGATGAATTCAGCAAACTGCTAC 420
Db 121 LysAspAlaIleLysLysLysPheThrGlyIleLysHisGluTrpGlnValAsnGlyLeu 140

QY 421 GAGGAGGTCAAGGACCGCTGCACCTGGCAGAGCAAGCTGGGGGCGAGTGGGTCATCTCC 480
Db 141 AspAspIleLysAspArgSerThrLeuGlyLysLeuGlyLysValValSer 160

QY 481 CTGAGGGCAAGCTTTG 498
Db 161 LeuGluGlyLysProLeu 166

RESULT 10
Q6NZW3 PRELIMINARY; PRT; 166 AA.
AC Q6NZW3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cofilin 2 (Muscle).
GN Name=cfl2;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
TI TISSUE=Embryo;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RC TISSUE=Embryo;
RA Director MGC Project;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC065947; AAH65947.1; -
DR HSP; P60982; IAK6.
DR ZFIN; ZDB-GENE-040426-1815; cfl2.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003779; F:actin binding; IEA.
DR InterPro; IPR002108; Actbind_cofln.
DR Pfam; PF00241; Cofilin_ADF; 1.
DR PRINTS; PR00006; COFILIN.
DR ProDom; PD002129; Actbind_cofln; 1.
DR SMART; SM00102; ADF; 1.
DR PROSITE; PS00325; ACTIN_DEPOLYMERIZING; 1.
DR SEQUENCE 166 AA; 18568 MW; 795942E0F8F0A2D6 CRC64;
SQ

Alignment Scores:

Pred. No.: 1.67e-51 Length: 166
Score: 693.00 Matches: 133
Percent Similarity: 89.76% Conservative: 16
Best Local Similarity: 80.12% Mismatches: 17
Query Match: 76.91% Indels: 0
DB: 2 Gaps: 0

US-10-649-952A-2 (1-501) x Q6NZW3 (1-166)

QY 1 ATGGCTCGGTGGTGGTCTCTGATGTCATCAAGGTGTTCAACGACATGAAGTG 60
Db 1 MetAlaSerGlyValThrValSerAspGluValIleLysValPheAsnAspMetLysVal 20

QY 61 CGTAAGTCTTCAACCCAGAGAGAGTGAAGAGCGCAAGAGCGGTCTCTTCGCTG 120
Db 21 ArgLysSerSerSerAspGluValLysLysArgLysLysAlaValLeuPheCysLeu 40

QY 121 AGTGAGGACAAAGAACATCATCTCGGAGGAGGCAAGGAGATCCTGGTGGCGATGTG 180
Db 41 SerAspAspLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 60

QY 181 GGCCAGACTGTCAGGATCCCTACGCCACCTTTGTCAAGATGCTGCCAGATAAGACTGC 240
Db 61 GlyAspSerValAspAspProTyrAlaCysPheValLysLeuLeuProLeuAsnAspCys 80

QY 241 CGCTATGCCCTCTATGATGCAACCTATGAGACCAAGGAGGAGCAAGGAGGATCTGGTG 300
Db 81 ArgTyrGlyLeuTyrAspAlaThrTyrGluThrLysGluSerLysLysGluAspLeuVal 100

QY 301 TTTATCTTCTGGGCCCCGAGTCTGCGCCCTTAAGAGCAAAATGATTATGCGAGTCC 360
Db 101 PheIlePheTyrAlaProGluGlyAlaProLeuLysSerLysMetIleTyrAlaSerSer 120

QY 361 AAGGAGCCATCAAGAGAGCTGACAGGATCAAGGATCAAGATGAATTGCAAGCAAACTGCTAC 420
Db 121 LysAspAlaIleLysLysPheThrGlyIleLysHisGluThrGluValAsnGlyLeu 140

QY 421 GAGGAGGTCAAGGACCGTGCACCTGCGAGAGCTGGCGGAGCTGGCGGAGTCTATCTCC 480
Db 141 AspAspIleGlnAspArgSerThrLeuAlaGluLysLeuGlyGlyAsnValValSer 160

QY 481 CTGGAGGCGCAAGCCCTTTG 498
Db 161 LeuGluGlyArgProLeu 166

RESULT 11

Q6NX11 PRELIMINARY; PRT; 168 AA.

AC Q6NX11; ID Q6NX11; DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DE Hypothetical protein MGC76274.
GN Name=MGC76274;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8364;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madao A., Rodriguez S., Sanchez A.,
RA Whiting M., Madao A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Gerhard D.S.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC067328; AAH67328.1; -.
DR HSSP; P60982; IAK6.

DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003779; F:actin binding; IEA.
DR InterPro; IPR002108; Actbind_cofin.
DR Pfam; PF00241; Cofilin_ADF; 1.
DR PRINTS; PR00006; COFILIN.
DR PRODom; PD002129; Actbind_cofin; 1.
DR SMART; SM00102; ADF; 1.
DR PROSITE; PS00325; ACTIN_DEPOLYMERIZING; 1.
KW Hypothetical protein.
SQ SEQUENCE 168 AA; 19073 MW; 14AB09FF9616496A CRC64;

Alignment Scores:

Pred. No.: 1.49e-48 Length: 168
Score: 659.00 Matches: 130
Percent Similarity: 83.13% Conservative: 8
Best Local Similarity: 78.31% Mismatches: 28
Query Match: 73.14% Indels: 0
DB: 2 Gaps: 0

US-10-649-952A-2 (1-501) x Q6NX11 (1-168)

QY 1 ATGGCTCGGTGGTGGTCTCTGATGTCATCAAGGTGTTCAACGACATGAAGTG 60
Db 1 MetAlaSerGlyValMetValSerAspAspValIleLysValPheAsnAspMetLysVal 20

QY 61 CGTAAGTCTTCAACCCAGAGAGTGAAGAGCGCAAGAGCGGTCTCTTCGCTG 120
Db 21 ArgHisGlnLeuSerProGluGluAlaLysLysArgLysLysAlaValPheCysLeu 40

QY 121 AGTGAGGACAAAGAACATCATCTCGGAGGAGGCAAGGAGATCCTGGTGGCGATGTG 180
Db 41 SerGluAspLysLysMetIleLysLysLysLysLysLysLysLysLysLysLys 60

QY 181 GGCCAGACTGTCAGATCCCTACGCCACCTTTGTCAAGATGCTGCCAGATAAGACTGC 240
Db 61 GlyCysAsnValAspAspProTyrLysAlaPheValLysMetLeuProArgAsnAspCys 80

QY 241 CGCTATGCCCTCTATGATGCAACCTATGAGACCAAGGAGGAGGAGGATCTGGTG 300
Db 81 ArgTyrAlaLeuTyrAspAlaLeuTyrGluThrLysGluThrLysLysGluAspLeuVal 100

QY 301 TTTATCTTCTGGGCCCCGAGTCTGCGCCCTTAAGAGCAAAATGATTATGCGAGTCC 360
Db 101 PheValPheTyrAlaProGluGluAlaSerLeuLysSerLysMetIleTyrAlaSerSer 120

QY 361 AAGGAGCCATCAAGAGAGCTGACAGGATCAAGGATCAAGATGAATTGCAAGCAAACTGCTAC 420
Db 121 LysAspAlaIleLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 140

QY 421 GAGGAGGTCAAGGACCGTGCACCTGCGAGAGCTGGCGGAGCTGGCGGAGTCTATCTCC 480
Db 141 GluAspIleAsnAspProCysAsnLeuAlaGluLysLeuGlyGlySerThrValIleSer 160

QY 481 CTGGAGGCGCAAGCCCTTTG 498
Db 161 LeuGluGlyArgProLeu 166

[illegible]

DR Pfam; PF00241; Cofilin_ADF; 1.
 DR PRINTS; PR00006; COFILIN.
 DR ProDom; PD002129; Actbind_cofin; 1.
 DR SMART; SM00102; ADF; 1.
 DR PROSITE; PS00325; ACTIN DEPOLYMERIZING; 1.
 KW Actin-binding; Cytoskeleton; Nuclear protein; Phosphorylation.
 FT DOMAIN 30 34
 FT DOMAIN 106 125 Actin-binding (Potential).
 SQ SEQUENCE 168 AA; 19066 MW; F3A4D8635A3683D6 CRC64;

Alignment Scores:
 Pred. No.: 1.1e-47 Length: 168
 Score: 649.00 Matches: 125
 Percent Similarity: 84.76% Conservative: 14
 Best Local Similarity: 76.22% Mismatches: 25
 Query Match: 72.03% Indels: 0
 DB: 1 Gaps: 0

US-10-649-952A-2 (1-501) x COFI_XENLA (1-168)

QY 1 ATGGCTCCGGTGGCTGCTCTGATGGTCTCATCAAGGTGTTCAAGCATCAAGGTG 60
 DB 1 MetAlaSerGlyValMetValSerAspValIleLysValPheAsnGluMetCysVal 20

QY 61 CGTAAGTCTTCAAGCCCAAGAGAGGTGAAGAGCGCAAGAGCGGTCTCTTGGCTG 120
 DB 21 ArgHisGlnLeuSerProGluAspAlaLysLysArgLysLysAlaValPheCysLeu 40

QY 121 AGTGAAGACAGAGACATCATCTGAGAGGCGCAAGAGATCTGGTGGCGATGTG 180
 DB 41 SerAspLysLysThrIleLeuGluProGlyLysGluLeuGlnGlyAspIle 60

QY 181 GGCCAGACTGCGAGCTCCCTAGCCACCTTCTCAAGATGCTGCCAGATAAGAGTGC 240
 DB 61 GlyCysAsnValGluAspProTyrLysThrPheValLysMetLeuProArgAsnAspCys 80

QY 241 CGCTATGCCCTCTATGATGCAACCTATGAGACCAAGAGAGCAAGAGGAGATCTGGT 300
 DB 81 ArgTyrAlaLeuTyrAspAlaLeuTyrGluThrLysGluThrLysLysGluAspLeuVal 100

QY 301 TTTATCTTGGGCCCCGAGTCTGGCCCCCTTAAGAGCAAAATGATTTATGCCAGTCC 360
 DB 101 PheValPheTyrAlaProGluGluAlaSerLeuLysSerLysMetIleTyrAlaSer 120

QY 361 AAGAGCGCCATCAAGAGAACTGACAGGATCAAGCATGAATTGCAAGCAAACTGCTAC 420
 DB 121 LysAspAlaIleLysLysArgLeuProGlyIleLysHisGluThrPheGlnIleAsnThrTyr 140

QY 421 GAGAGGTCAAGGACCGCTGCACCTGCGCAGAGAGCTGGGGGCGAGTGGCGTCACTCC 480
 DB 141 GluAspValAsnAspProCysAsnLeuAlaAspLysLeuGlyGlyAsnThrValValSer 160

QY 481 CTGAGGCGCAAG 492
 DB 161 LeuGluGlyLys 164

RESULT 14
 Q6TH32 PRELIMINARY; PRT; 165 AA.
 AC Q6TH32;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Muscle cofilin 2.
 GN Name=cfil2; Synonyms=CFL2;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Bania.
 OK NCBI_taxid=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney marrow;

RA Song H.D., Wu X.Y., Sun X.J., Zhou Y., Liu T.X., Deng M., Zhang G.W.,
 RA Sheng Y., Chen Y., Ruan Z., Jiang C.L., Fan H.Y., Zou L.I.,
 RA Kanki J.P., Look A.T., Chen Z.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY398324; AAQ97757.1; -.
 DR HSSP; P60982; 1AK6.
 DR ZFIN; ZDB-GENE-030131-215; cfl21.
 DR GO; GO:0005622; C:intracellular; IEA.
 DR GO; GO:0003779; F:actin binding; IEA.
 DR InterPro; IPR002108; Actbind_cofin.
 DR Pfam; PF00241; Cofilin_ADF; 1.
 DR PRINTS; PR00006; COFILIN.
 DR ProDom; PD002129; Actbind_cofin; 1.
 DR SMART; SM00102; ADF; 1.
 DR PROSITE; PS00325; ACTIN DEPOLYMERIZING; 1.
 SQ SEQUENCE 165 AA; 18771 MW; 3FD3F8F542E2A707 CRC64;

Alignment Scores:
 Pred. No.: 1.2e-45 Length: 165
 Score: 625.50 Matches: 125
 Percent Similarity: 85.03% Conservative: 17
 Best Local Similarity: 74.85% Mismatches: 20
 Query Match: 69.42% Indels: 5
 DB: 2 Gaps: 2

US-10-649-952A-2 (1-501) x Q6TH32 (1-165)

QY 1 ATGGCTCCGGTGGCTGCTCTGATGGTGTCTCATCAAGGTGTTCAAGCATCAAGGTG 60
 DB 1 MetAlaSerGlyValThrValGluGluThrValLeuThrValPheAsnGluMetLysVal 20

QY 61 CGTAAGTCTTCAAGCCCAAGAGAGGTGAAG---AAGCGCAAGAGCGGTCTCTTCTGC 117
 DB 21 ArgLysAlaHisCysAsnGluGluGluLysSerLysArgLysLysAlaValMetPheCys 40

QY 118 CTGAGTGAGGACAAAGAAACATCATCTCGAGAGGGCAAGAGATCTCTGGTGGCGAT 177
 DB 41 LeuSerAspLysLysHisIleMetGluGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 60

QY 178 GTGGGCCAGACTGCGAGATCCCTAGCCACCTTGTCAAGATGCTGCCAGATAAGAC 237
 DB 61 GluGly-----AspProTyrLeuLysPheValLysMetLeuProAsnAsp 76

QY 238 TGCGCGTATCCCTCTATGATCAACCTATGAGACCAAGAGAGAGAGAGGAGTCTG 297
 DB 77 CysArgTyrAlaLeuTyrAspAlaThrTyrGluThrLysGluThrLysLysGluAspLeu 96

QY 298 GTGTTTATCTTCTGGCCCCCGAGTCTGCGCCCCCTTAAGAGCAAAATGATTTATGCCAGC 357
 DB 97 ValPheIlePheThrAlaProGluSerAlaProLeuLysSerLysMetIleTyrAlaSer 116

QY 358 TCAAGAGCCCATCAAGAAAGCTGACAGGGATCAAGCATGAATTGCAAGCAAACTGC 417
 DB 117 SerLysAspAlaIleLysLysPheThrGlyIleLysHisGluThrPheGlnValAsnGly 136

QY 418 TAGCAGGAGTCAAGGACCGCTGCACCTGCGCAGAGAGCTGGGGGCGAGTGGGTGTCATC 477
 DB 137 MetAspLysLysAspArgLysThrLeuAlaGluLysLeuGlyAlaSerValVal 156

QY 478 TCCTTGAGGGCGAGCGCTTTG 498
 DB 157 SerLeuGluGlyLysProLeu 163

RESULT 15
 DEST CHICK
 ID DEST CHICK STANDARD; PRT; 164 AA.
 AC P18359;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 25-JAN-2005 (Rel. 46, Last sequence update)
 DT 25-JAN-2005 (Rel. 46, Last annotation update)
 DE Desitin (Actin-depolymerizing factor) (ADF).
 GN Name=DSN; Synonyms=DSN;
 OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 100-110 AND 115-133.
RC TISSUE=Brain;
RX MDLLINE=91027754; PubMed=2223773;
RA Adams M.E., Minamide L.S., Duester G., Bamberg J.R.;
RT "Nucleotide sequence and expression of a cDNA encoding chick brain
RL actin depolymerizing factor.";
RL Biochemistry 29:7414-7420(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MDLLINE=91027755; PubMed=1699599;
RA Abe H., Endo T., Yamamoto K., Obinata T.;
RT "Sequence of cDNAs encoding actin depolymerizing factor and cofilin of
RT embryonic chicken skeletal muscle: two functionally distinct actin-
RT regulatory proteins exhibit high structural homology.";
RL Biochemistry 29:7420-7425(1990).
CC -1- FUNCTION: Actin-depolymerizing protein. Severs actin filaments (F-
CC actin) and binds to actin monomers (G-actin). Acts in a pH-
CC independent manner.
CC -1- SIMILARITY: Belongs to the actin-binding proteins ADF family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J02912; AAA48575.1; --
DR EMBL; M55660; AAA48573.1; --
DR PIR; A35702; A35702.
DR HSSP; P18282; IAK6.
DR InterPro; IPR002108; Actbind_cofin.
DR Pfam; PF00241; Cofilin_ADF; 1.
DR PRINTS; PR00006; COFILIN.
DR PRODOM; PD002129; Actbind_cofin; 1.
DR SMART; SM00102; ADF; 1.
DR PROSITE; PS00325; ACTIN DEPOLYMERIZING; 1.
KW Actin-binding; Direct protein sequencing.
FT INIT MET 0 By similarity.
FT DOMAIN 29 33 Nuclear localization signal (Potential).
FT DOMAIN 105 124 Actin-binding (Potential).
SQ SEQUENCE 164 AA; 18401 MW; 72747A1D43E6E3E9 CRC64;

Alignment Scores:
Pred. No.: 8.88e-45 Length: 164
Score: 615.50 Matches: 121
Percent Similarity: 84.24% Conservative: 18
Best Local Similarity: 73.33% Mismatches: 25
Query Match: 68.31% Indels: 1
DB: 1 Gaps: 1

US-10-649-952a-2 (1-501) x DEST_CHICK (1-164)

QY 4 GCCTCCGGTGGCTGCTCTGATGTCATCAAGGTGTTCAACGACATGAAGGTGCGT 63
DB 1 AlaSerGlyValGlnValAlaAspGluValCysArgIlePheTyrAspMetLysValArg 20

QY 64 AGCTCTCAACGCGAGAGGTGAAGAACGCGAAGCGGTGCTTTCTCCCTGAGT 123
DB 21 LysCysSerThrProGluGluValLysLysArgLysAlaValIlePheCysLeuSer 40

QY 124 GAGGCAAGAGACATCATCTGGAGGCGGCAAGAGATCCTGGTGGCGGATGCGC 183
DB 41 ProAspLysLysCysIleIleValGluGluGlyLysGluIleLeuValGlyAspValGly 60

QY 184 CAGACTGTCAGCATCCCTACGCCACCTTTGTCAAGATGCTGCCAGATAGGACTGCCGC 243

Db 61 valThrValThrAspProPheLysHisPheValGluMetLeuProGluLysAspCysArg 80
QY 244 TATGCCCTCTATGATCAACCTATGAGCAACGAGAGCAAGAGAGGAGGATCTGGTCTTT 303
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Db 121 AspAlaIleLysLysLysPheGlnGlyIleLysHisGluCysGlnAlaAsnGlyProGlu 140
QY 424 GAGGTCAAGGACCGCTGCCCTGGGAGAGAGCTGGGGGCGAGTGGGGTCATCTCCCTG 483
Db 141 AspLeuAsnArgAlaCys---IleAlaGluLysLysGlySerLeuValValAlaPhe 159
QY 484 GAGGGCAAGCCTTTG 498
Db 160 GluGlySerProVal 164

Search completed: May 13, 2005, 09:59:23
Job time : 140 secs

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: May 13, 2005, 09:48:26 ; Search time 30.5 Seconds
(without alignments)
2452.405 Million cell updates/sec

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Perfect score: 901
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: ; 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 1027090

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	628	69.7	127	4	US-09-513-999C-8059 Sequence 8059, Ap
2	606.5	67.3	165	4	US-09-513-999C-7957 Sequence 7957, Ap
3	354	39.3	86	4	US-09-513-999C-5489 Sequence 5489, Ap
4	287	31.9	69	4	US-09-513-999C-5488 Sequence 5488, Ap
5	242.5	26.9	146	4	US-09-513-999C-20627 Sequence 20627, A
6	188.5	20.9	154	4	US-09-513-999C-20627 Sequence 20627, A
7	149	16.5	30	1	US-08-184-252A-5 Sequence 5, Appli
8	149	16.5	30	5	PCT-US95-00601-5 Sequence 5, Appli
9	124	13.8	28	4	US-09-017-689A-4 Sequence 4, Appli
10	124	13.8	30	1	US-08-184-252A-6 Sequence 6, Appli
11	124	13.8	30	5	PCT-US95-00601-6 Sequence 6, Appli
12	120	13.3	350	2	US-09-123-851-3 Sequence 3, Appli

13	120	13.3	350	2	US-08-728-520-3	Sequence 3, Appli
14	118	13.1	272	4	US-09-252-991A-31152	Sequence 31152, A
15	117.5	12.7	481	4	US-09-949-016-9748	Sequence 9748, Ap
16	116	12.9	350	1	US-08-184-252A-2	Sequence 2, Appli
17	116	12.9	350	5	PCT-US95-00601-2	Sequence 2, Appli
18	115	12.8	383	4	US-09-252-991A-20625	Sequence 20625, A
19	114.5	12.4	214	4	US-09-252-991A-19397	Sequence 19397, A
20	114	12.7	156	4	US-09-252-991A-31875	Sequence 31875, A
21	109.5	11.8	228	4	US-09-252-991A-28381	Sequence 28381, A
22	108	12.0	141	4	US-09-252-991A-28438	Sequence 28438, A
23	107	11.9	114	4	US-09-252-991A-31192	Sequence 31192, A
24	107	11.9	220	4	US-09-252-991A-17636	Sequence 17636, A
25	107	11.5	267	4	US-09-252-991A-28620	Sequence 28620, A
26	106.5	11.8	171	4	US-09-252-991A-26927	Sequence 26927, A
27	106.5	11.5	173	4	US-09-252-991A-32359	Sequence 32359, A
28	106	11.8	216	4	US-09-252-991A-32065	Sequence 32065, A
29	106	11.8	266	4	US-09-252-991A-19128	Sequence 19128, A
30	106	11.8	299	4	US-09-252-991A-17588	Sequence 17588, A
31	106	11.8	529	4	US-09-252-991A-28641	Sequence 28641, A
32	105.5	11.7	172	4	US-09-252-991A-17765	Sequence 17765, A
33	105.5	11.7	242	4	US-09-252-991A-27672	Sequence 27672, A
34	105.5	11.4	699	4	US-09-252-991A-26231	Sequence 26231, A
35	105	11.7	234	4	US-09-252-991A-28621	Sequence 28621, A
36	104.5	11.6	121	4	US-09-252-991A-28679	Sequence 28679, A
37	104.5	11.6	196	4	US-09-252-991A-16779	Sequence 16779, A
38	104.5	11.6	268	4	US-09-252-991A-17943	Sequence 17943, A
39	104	11.5	144	4	US-09-252-991A-24476	Sequence 24476, A
40	104	11.5	191	4	US-09-252-991A-23902	Sequence 23902, A
41	103.5	11.5	320	4	US-09-252-991A-24634	Sequence 24634, A
42	103.5	11.5	343	2	US-09-123-851-1	Sequence 1, Appli
43	103.5	11.5	343	2	US-08-728-520-1	Sequence 1, Appli
44	103	11.4	228	4	US-09-252-991A-18111	Sequence 18111, A
45	103	11.4	414	4	US-09-252-991A-31151	Sequence 31151, A

ALIGNMENTS

RESULT 1
US-09-513-999C-8059
; Sequence 8059, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Giordano, J. Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 8059
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 122
; OTHER INFORMATION: Xaa=Ala or Thr
US-09-513-999C-8059

Alignment Scores:
Pred. No.: 7.36e-62
Score: 628.00
Percent Similarity: 98.44%
Best Local Similarity: 98.44%
Query Match: 69.70%
Indels: 1
Gaps: 0
Length: 127
Matches: 126
Conservative: 0
Mismatch: 1

US-10-649-952A-2 (1-501) x US-09-513-999C-8059 (1-127)

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Qy 61 CGTAAGTCTTCAACGCCAGAGAGGTGAAGAACGCGCAAGAGCGGTGCTCTTCTGCTG 120
Db 21 ArgLysSerSerThrProGluGluValLysLysArgLysLysAlaValLeuPheCysLeu 40
Qy 121 AGTGAGGACAGAGAACATCATCTCTGGAGAGGCGCAAGAGATCTGTGGGCGATGTG 180
Db 41 SerGluAspLysLysAsnIleLeuGluGluGlyLysGluIleLeuValGlyAspVal 60
Qy 181 GGCCAGAGCTGCGACGATCCCTAGCCACCTTTGTCAAGATGCTGCCAGATAAGGACTGC 240
Db 61 GlyGlnThrValAspAspProTyrAlaThrPheValLysMetLeuProAspLysAspCys 80
Qy 241 CGCTATGCGCTCTATGATCAACCTATGAGACCAAGGAGAGCAAGAGGAGTCTGGTG 300
Db 81 ArgTyrAlaLeuTyrAspAlaThrTyrGluThrLysGluSerLysLysGluAspLeuVal 100
Qy 301 TTTATCTTCTGGGCGCGGAGTCTGCGCCCTTAAAGCAAAATGATTATGCGAGTCC 360
Db 101 PheIlePheTrpAlaProGluSerAlaProLeuLysSerLysMetIleTyrAlaSerSer 120
Qy 361 AAGGACGCGCATCAAGAGAAGC 382
Db 121 Lys-***ProSerArgArgSer 127
RESULT 2
US-09-513-999C-7957
; Sequence 7957, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 7957
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-7957
Alignment Scores:
Pred. No.: 2,08e-59 Length: 165
Score: 606.50 Matches: 118
Percent Similarity: 83.73% Conservative: 21
Best Local Similarity: 71.08% Mismatches: 26
Query Match: 67.31% Indels: 1
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Qy 61 CGTAAGTCTTCAACGCCAGAGAGGTGAAGAACGCGCAAGAGCGGTGCTCTTCTGCTG 120
Db 21 ArgLysCysSerThrProGluGluIleLysLysArgLysLysAlaValIlePheCysLeu 40
Qy 121 AGTGAGGACAGAGAACATCATCTCTGGAGAGGCGCAAGAGATCTGTGGGCGATGTG 180
Db 41 SerAlaAspLysLysCysIleValGluGluGlyLysGluIleLeuValGlyAspVal 60
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Qy 181 GGCCAGAGCTGCGACGATCCCTAGCCACCTTTGTCAAGATGCTGCCAGATAAGGACTGC 240
Db 61 GlyValThrIleThrAspProPheLysHisPheValGlyMetLeuProGluLysAspCys 80
Qy 241 CGCTATGCGCTCTATGATCAACCTATGAGACCAAGGAGAGCAAGAGGAGTCTGGTG 300
Db 81 ArgTyrAlaLeuTyrAspAlaSerPheGluThrLysGluSerArgLysGluGluLeuMet 100
Qy 301 TTTATCTTCTGGGCGCGGAGTCTGCGCCCTTAAAGCAAAATGATTATGCGAGTCC 360
Db 101 PhePheLeuTrpAlaProGluLeuAlaProLeuLysSerLysMetIleTyrAlaSerSer 120
Qy 361 AAGGACGCGCATCAAGAGAAGCTGACAGGATCAAGCATCAATTGCAAGCAAACTGCTAC 420
Db 121 LysAspAlaIleLysLysLysPheGlnGlyIleLysHisGluCysGlnAlaAsnGlyPro 140
Qy 421 GAGGAGTCAAGGACCGCTGCAACCTGCGAGAGAGCTGGGGGCGAGTGGCGTCATCTCC 480
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Qy 481 CTGGAGGCGCAAGCCTTTG 498
Db 160 PheGluGlyCysProVal 165
RESULT 3
US-09-513-999C-5489
; Sequence 5489, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 5489
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-5489
Alignment Scores:
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Best Local Similarity: 77.91% Mismatches: 9
Query Match: 39.29% Indels: 0
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US-10-649-952A-2 (1-501) x US-09-513-999C-5489 (1-86)
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Db 21 ArgLysSerSerThrGlnGluIleLysLysArgLysLysAlaValLeuPheCysLeu 40
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Db 41 SerAspAspLysArgGlnIleIleValGluGluAlaLysGlnIleLeuValGlyAspIle 60
Qy 181 GGCCAGAGCTGCGACGATCCCTAGCCACCTTTGTCAAGATGCTGCCAGATAAGGACTGC 240
Db 61 GlyAspThrValGluAspProTyrThrSerPheValLysLeuProLeuAsnAspCys 80
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QY 241 CGCTATGCCCTCTATGAT 258
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RESULT 4
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; Sequence 5488, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59. US2. REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 5488
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-5488

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QY 172 GCGATGTGGCCAGACTGTGACAGATCCCTACGCCACCTTCTCAAGATGCTGCCAGAT 231
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QY 232 AAGGACTGCGCTATGCCCTCTATGAT 258
Db 61 AsnAspCysArgTyraLeuTyraep 69

RESULT 5
US-09-248-796A-20627
; Sequence 20627, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 20627
; LENGTH: 146
; TYPE: PRT

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; ORGANISM: Candida albicans
US-09-248-796A-20627

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Percent Similarity: 59.57% Conservative: 38
Best Local Similarity: 32.62% Mismatches: 36
Query Match: 26.91% Indels: 21
DB: 4 Gaps: 3

US-10-649-952A-2 (1-501) x US-09-248-796A-20627 (1-146)

QY 13 GTGGCTGTCTGTGATGGTGTCTCATCAAGGTGTTCAAGACATGAAGTGCCTAAGTCTTCA 72
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QY 73 AGCCAGAGGAGGTGAAGAGGCGCAAGAGGCGGTCTCTTCTGCTGAGTGAGGACAG 132
Db 26 -----LeuGlyArgLysTyrlsPheValIlePheThrLeuAsnAspGluLys 41

QY 133 AAGAACATCATCTGGAGAGGCGCAAGGAGATCCTGGTGGCGATGTGGGCCAGACTGTC 192
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QY 193 GAGATCCCTACGCCACCTTGTCAAGATGCTGCCAGATAAGAGTGCCTATGCCCTC 252
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QY 253 TATGATGCAACCTATCAGACC-----AAGGAGACGAAGAAGAGGATCTGGTGTTC 306
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QY 307 TTCTGGGCCCCGAGTCTGCCCTTAAAGAGCAAAATGATTATGCCAGCTCCAAGGAC 366
Db 92 ThrTrpSerProAspThrAlaProValArgAlaLysMetValTyraLysSerLysAsp 111

QY 367 GCCATCAAGAAGAAGCTGACAGGATCAAGGATCAAGCAATTCGAAGCAAACTGCTACGAGGAG 426
Db 112 SerLeuArgArgAlaLeuAsnGlyValAlaAlaAspValGlnArgThrAspPheSerGlu 131

QY 427 GTC 429
Db 132 Val 132

RESULT 6
US-09-723-830-2
; Sequence 2, Application US/09723830
; Patent No. 6458930
; GENERAL INFORMATION:
; APPLICANT: Nislow, Corey
; APPLICANT: Wong, Kee
; TITLE OF INVENTION: Aspergillus fumigatus Cofilin
; FILE REFERENCE: 1039
; CURRENT APPLICATION NUMBER: US/09/723,830
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-09-723-830-2

Alignment Scores:
Pred. No.: 1.38e-12 Length: 154
Score: 188.50 Matches: 50
Percent Similarity: 50.60% Conservative: 34
Best Local Similarity: 30.12% Mismatches: 57
Query Match: 20.92% Indels: 25
DB: 4 Gaps: 7

US-10-649-952A-2 (1-501) x US-09-723-830-2 (1-154)

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Percent Similarity: 96.67% Conservative: 0
Best Local Similarity: 96.67% Mismatches: 1
Query Match: 16.54% Indels: 0
DB: 5 Gaps: 0

US-10-649-952A-2 (1-501) x PCT-US95-00601-5 (1-30)

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Db 1 PheilePheTrpAlaProGluSerAlaProLeuLysSerLysMetIleTyAlaSerSer 20
QY 361 AAGAGCCCATCAAGAAGAAGCTGACAGGG 390
Db 21 LysAspAlaIleLysLysPheThrGly 30

RESULT 9

US-09-017-689A-4
; Sequence 4, Application US/09017689A
; Patent No. 6413940
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, Paul
; TITLE OF INVENTION: PHARMACEUTICALLY ACTIVE AGENTS THAT
; IMPED THE FORMATION OF AMYLOID BY IMPEDING THE GENESIS OF
; DMS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/017,689A
FILING DATE: 03-Feb-1998
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/038,694
FILING DATE: 07-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 018792/0125
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-017-689A-4

Alignment Scores:
Pred. No.: 1,25e-05 Length: 28
Score: 124.00 Matches: 24
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 96.00% Mismatches: 0
Query Match: 13.76% Indels: 0
DB: 4 Gaps: 0

US-10-649-952A-2 (1-501) x US-09-017-689A-4 (1-28)

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Db 1 AsnIleIleLeuGluGluGlyLysAspIleLeuValGlyAspValGlyGlnThrValasp 20
QY 196 GATCCCTACGCCACC 210
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Db 21 AspProTyAlaThr 25

RESULT 10

US-08-184-252A-6
; Sequence 6, Application US/08184252A
; Patent No. 5573935
; GENERAL INFORMATION:
; APPLICANT: Beeler, John F.
; APPLICANT: Laroche, William
; APPLICANT: Aaronson, Stuart A.
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE A6
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens Olson & Bear
; STREET: 620 Newport Center Drive, Sixteenth Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/184,252A
FILING DATE: 18-JAN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Israel, Ned A.
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH084.001A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal

US-08-184-252A-6

Alignment Scores:
Pred. No.: 1,28e-05 Length: 30
Score: 124.00 Matches: 22
Percent Similarity: 90.00% Conservative: 5
Best Local Similarity: 73.33% Mismatches: 3
Query Match: 13.76% Indels: 0
DB: 1 Gaps: 0

US-10-649-952A-2 (1-501) x US-08-184-252A-6 (1-30)

QY 301 TTTATCTTCTGGGCCCCGAGTCTGGCCCTTAAGAGCAAAATGATTATGCCAGTCC 360
Db 1 PheileLeuTrpAlaProAspSerAlaProIleLysSerLysMetTyrThrSerThr 20
QY 361 AAGAGCCCATCAAGAAGAAGCTGACAGGG 390
|||||
Db 21 LysAspSerIleLysLysLeuValGly 30

RESULT 11

PCT-US95-00601-6
; Sequence 6, Application PCT/TUS9500601
; GENERAL INFORMATION:

APPLICANT: United States of America Department of Health and Human
APPLICANT: Services
TITLE OF INVENTION: PROTEIN TYROSINE KINASE A6
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobel, Martens Olson & Bear
STREET: 620 Newport Center Drive, Sixteenth Floor
CITY: Newport Beach
STATE: CA
COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00601
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned A.
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NH084.001A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
PCT-US95-00601-6

Alignment Scores:
Pred. No.: 1.29e-05 Length: 30
Score: 124.00 Matches: 22
Percent Similarity: 90.00% Conservative: 5
Best Local Similarity: 73.33% Mismatches: 3
Query Match: 13.76% Indels: 0
DB: 5 Gaps: 0

US-10-649-952A-2 (1-501) x PCT-US95-00601-6 (1-30)

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Qy 361 AAGGACGCCATCAAGAAGAGCTGACAGGG 390
Db 21 LysaspSerIleLysLysLysLeuValGly 30

RESULT 12
US-09-123-851-3
Sequence 3, Application US/09123851
Patent No. 5958405
GENERAL INFORMATION:
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: A NOVEL HUMAN PROTEIN TYROSINE KINASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/123,851
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/728,520
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0136 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 451482
US-09-123-851-3

Alignment Scores:
Pred. No.: 8.83e-05 Length: 350
Score: 120.00 Matches: 34
Percent Similarity: 55.56% Conservative: 36
Best Local Similarity: 26.98% Mismatches: 40
Query Match: 13.32% Indels: 16
DB: 2 Gaps: 6

US-10-649-952A-2 (1-501) x US-09-123-851-3 (1-350)

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Db 11 GluAspValLysGlu-----IlePheAlaArgAlaArgAsnGlyLysTyr 25
Qy 139 ATCATCTCTGAG-----GAGGGCAAGGAGATCTGTGGCGCATGTGGGCCAG-- 186
Db 26 ArgLeuLeuLysIleSerIleGluAsnGluGlnLeuValIleGlySerTyrSerGlnPro 45
Qy 187 -----ACTGTCGACGATCCTACGCCACCTTTGTC---AAGATGTCGCCAGATAAGGAC 237
Db 46 SerAspSerTrpAspLysAspTyrAspSerPheValLeuProLeuLeuGluAspLysGln 65
Qy 238 TGGCGTATCCCTCTATGATGCAACCTATGACACCAAGAGAGAGAGAGGAGGATCTG 297
Db 66 ProCysTyrIleLeuPhe-----ArgLeuAspSerGlnAsnAlaGlnGlyTyrGluTrp 83
Qy 298 GTGTTTATCTTCTGGGCCCCGAGTCTGCGCCCTTAAGAGCAAAATGATTATGCCAGC 357
Db 84 IlePheIleAlaTrpSerProAspHisSerHisValArgGlnLysMetLeuTyrAlaAla 103
Qy 358 TCCAAGGACGCCATCAAGAAGAAGCTGACAGC-----ATCAGCATGAATTGCAAGCA 411
Db 104 ThrArgAlaThrLeuLysLysGluPheGlyGlyHisIleLysAspGluValPheGly 123
Qy 412 AACTGCTACGAGGAGTTC 429
Db 124 ThrValLysGluAspVal 129

RESULT 13
US-08-728-520-3
Sequence 3, Application US/08728520
Patent No. 5994112
GENERAL INFORMATION:
APPLICANT: Goli, Surya K.


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Qy      79  CTGCGCTTGAAGACTTACCACTTCATCGT  47
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Db      393  MetArgLeuProThrArgAlaProThrAlaArg  403

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Job time : 32.5 secs

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Search completed: May 13, 2005, 10:01:42
Job time : 32.5 secs

US-10-649-952A-2 (1-501) x US-09-949-016-9748 (1-481)

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430	QY	TG	ACCTCTCT	CGTAG	CAGTTT	CGTTC	TGCA	ATTCA	TGCTTGA	TCCCTGT	CAGCTTCTCT	TCTTGA	371	
293	Db	Pro	Pro	Pro	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	297	
370	QY	TG	CGCTCTCT	TGG	AGCTGG	GCATAA	TCA	TATTT	TGCTCTT	TAA	GGGCG	CAGACTCG	GGGGCCC	311
298	Db	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	302
310	QY	AGA	GATAA	AC	CAC	CAGATC	CTCTCT	TCTT	TGCTCT	CTCT	CTCT	CTCT	CTCT	275
303	Db	Pro	Arg	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	319
274	QY	---	TGCTCT	CAT	AGTTT	GCAT	CAT	AGAGG	GCATAG	CGGCAGT	CGTCTTATCT	TGGCAG	CATCT	218
320	Db	Arg	Trp	Pro	Arg	Arg	Leu	Gln	Ser	Thr	Thr	Pro	Arg	339
217	QY	TC	ACAA	AGGTG	---	---	---	---	---	---	---	---	---	173
340	Db	---	Ser	Ala	trp	Phe	Leu	Ser	Gly	Arg	Ser	Ala	Gln	358
172	QY	---	CC	AC	GAG	TCTCT	CTT	GGC	CTCT	CTCT	CC	CAG	GAT	137
359	Db	Pro	Ala	Ala	Leu	Ala	Pro	Leu	Pro	Pro	Pro	Pro	Ala	378
136	QY	---	TC	TCT	TGT	CTCT	CACT	CAGG	CAG	AGC	ACCG	CTTCTT	TTC	80
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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: May 13, 2005, 09:50:51 ; Search time 106.5 Seconds
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3142.909 Million cell updates/sec

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Perfect score: 901
Sequence: 1 atggcctccggtgtggtgtg.....tggagggaagcctttgtga 501

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1432185 seqs, 334051727 residues

Total number of hits satisfying chosen parameters: 2864370

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPCL=0 -LOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCAUGN=200 -THR SCORE=pct -THR MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10649952 @CGN 1 1 199 @runat 13052005_102650_27349
-NCPU=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-XGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications AA:
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US05_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
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11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
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16: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
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18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query

No.	Score	Match	Length	DB	ID	Description
1	846	93.9	166	16	US-10-649-952A-1	Sequence 1, Appl
2	764	84.8	149	16	US-10-408-765A-2270	Sequence 2270, Ap
3	702	77.9	166	14	US-10-205-342-21	Sequence 21, Appl
4	699	77.6	166	14	US-10-205-823-72	Sequence 72, Appl
5	699	77.6	166	16	US-10-408-765A-1910	Sequence 1910, Ap
6	699	77.6	205	15	US-10-158-034-93	Sequence 93, Appl
7	557.5	61.9	148	16	US-10-408-765A-2351	Sequence 2351, Ap
8	460	51.1	129	15	US-10-158-034-94	Sequence 94, Appl
9	450	49.9	156	15	US-10-158-034-68	Sequence 68, Appl
10	273	30.3	106	15	US-10-264-049-4340	Sequence 4340, Ap
11	267.5	29.7	143	15	US-10-369-493-22293	Sequence 22293, A
12	253.5	28.1	141	16	US-10-263-255-2	Sequence 2, Appl
13	245.5	27.2	141	16	US-10-263-255-4	Sequence 4, Appl
14	239.5	26.6	139	15	US-10-424-599-186070	Sequence 186070, A
15	230	25.5	60	14	US-10-029-386-30107	Sequence 30107, A
16	230	25.5	190	15	US-10-369-493-2272	Sequence 2272, Ap
17	227	25.2	145	15	US-10-425-114-37040	Sequence 37040, A
18	227	25.2	161	15	US-10-425-114-59591	Sequence 59591, A
19	227	25.2	171	15	US-10-425-114-39098	Sequence 39098, A
20	227	25.2	179	15	US-10-425-114-41223	Sequence 41223, A
21	227	25.2	179	15	US-10-425-114-41223	Sequence 41223, A
22	227	25.2	179	15	US-10-425-114-41223	Sequence 41223, A
23	227	25.2	179	15	US-10-425-114-51312	Sequence 51312, A
24	227	25.2	179	15	US-10-425-114-57582	Sequence 57582, A
25	227	25.2	179	15	US-10-425-114-59194	Sequence 59194, A
26	227	25.2	179	15	US-10-425-114-59883	Sequence 59883, A
27	227	25.2	179	15	US-10-425-114-66714	Sequence 66714, A
28	227	25.2	179	15	US-10-425-114-6765	Sequence 6765, A
29	227	25.2	179	15	US-10-425-114-72052	Sequence 72052, A
30	227	25.2	179	15	US-10-425-114-72097	Sequence 72097, A
31	224.5	24.9	139	16	US-10-767-701-45854	Sequence 45854, A
32	223.5	24.8	194	16	US-10-767-701-43979	Sequence 43979, A
33	221	24.5	139	15	US-10-250-613-9	Sequence 9, Appl
34	221	24.5	157	15	US-10-425-114-59062	Sequence 59062, A
35	221	24.5	173	15	US-10-425-114-66010	Sequence 66010, A
36	221	24.5	176	15	US-10-425-114-69864	Sequence 69864, A
37	221	24.5	177	15	US-10-425-114-44953	Sequence 44953, A
38	221	24.5	177	15	US-10-425-114-48026	Sequence 48026, A
39	221	24.5	177	15	US-10-425-114-48329	Sequence 48329, A
40	221	24.5	177	15	US-10-425-114-49519	Sequence 49519, A
41	221	24.5	177	15	US-10-425-114-53265	Sequence 53265, A
42	221	24.5	177	15	US-10-425-114-53325	Sequence 53325, A
43	221	24.5	177	15	US-10-425-114-66577	Sequence 66577, A
44	221	24.5	177	15	US-10-425-114-66602	Sequence 66602, A
45	221	24.5	181	15	US-10-425-114-69951	Sequence 69951, A

ALIGNMENTS

RESULT 1

US-10-649-952A-1
; Sequence 1, Application US/10649952A
; Publication No. US20040157326A1
; GENERAL INFORMATION:
; APPLICANT: DAIICHI SUNTORY PHARMA CO., LTD.
; APPLICANT: DAIICHI SUNTORY PHARMA CO., LTD.
; APPLICANT: Miura, Kenju
; APPLICANT: Haruyama, Munetada
; APPLICANT: Kodama, Shio
; TITLE OF INVENTION: Promoters of the growth and/or differentiation of hematopoietic stem cells and/or hematopoietic progenitors
; FILE OF INVENTION: 58777.000013
; FILE REFERENCE: 58777.000013
; CURRENT APPLICATION NUMBER: US/10/649,952A
; CURRENT FILING DATE: 2003-08-28
; PRIOR APPLICATION NUMBER: PCT/JP02/13862
; PRIOR FILING DATE: 2002-12-27
; PRIOR APPLICATION NUMBER: JAPAN 400330/2001
; PRIOR FILING DATE: 2001-12-28
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 1

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; LENGTH: 166
; TYPE: PRT
; ORGANISM: Human
US-10-649-952A-1
Alignment Scores:
Pred. No.: 1.09e-73 Length: 166
Score: 846.00 Matches: 166
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 93.90% Indels: 0
DB: 16 Gaps: 0

US-10-649-952A-2 (1-501) x US-10-649-952A-1 (1-166)
Qy 1 ATGCCCTCGGTGGCTGCTCTGATGGTGTCTCAAGGTGTTCAAGCATGAAGGTG 60
Db 1 MetAlaSerGlyValAlaValSerAspGlyValIleLysValPheAsnAaspMetLysVal 20
Qy 61 CGTAAGTCTTCAACGCCAGAGAGGTGAAGAGCGCAAGAGCGGTGCTCTTCTGCTG 120
Db 21 ArgLysSerSerThrProGluGluValLysLysArgLysLysAlaValLeuPheCysLeu 40
Qy 121 AGTGAGGACAAAGAAACATCATCTCGAGGAGGCGCAAGAGATCTCGTGGCGATGTG 180
Db 41 SerGluAspLysLysAsnIleLeuGluGluGlyLysGluIleLeuValGlyAspVal 60
Qy 181 GCCCAGACTGTCAGCATCCCTAGCCACCTTTGTCAGATGCTGCCAGATAAGACTGC 240
Db 61 GlyGlnThrValAspAspProTyAlaThrPheValLysMetLeuProAspLysAspCys 80
Qy 241 CGCTATCCCTCTATGATGCAACCTATGACACCAAGAGAGAGAGAGAGGATCTCGTG 300
Db 81 ArgTyralaLeuTyralaLeuTyralaLeuTyralaLeuTyralaLeuTyralaLeu 100
Qy 301 TTTATCTTCTGGGCCCCAGCTCTGCGCCCCCTTAAGAGCAAAATGATTATGCGAGTCC 360
Db 101 PheIlePheTrpAlaProGluSerAlaProLeuLysSerLysMetIleTyAlaSerSer 120
Qy 361 AAGAGCGCATCAAGAAAGACTGACAGGGATCAAGCATGATGATGCAAGCAAACTGCTAC 420
Db 121 LysAspAlaIleLysLysLysLeuThrGlyIleLysHisGluLeuGlnAlaAsnCysTy 140
Qy 421 GAGGAGTCAAGGACCGCTGACCCCTGCGAGAGAGCTGGGGGCGAGTGGGCTCATCTCC 480
Db 141 GluGluValLysAspArgCysThrLeuAlaGluLysLeuGlySerAlaValIleSer 160
Qy 481 CTGAGGGGCAAGCCTTTG 498
Db 161 LeuGluGlyLysProLeu 166

RESULT 2
US-10-408-765A-2270
; Sequence 2270, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Wainock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2270
; LENGTH: 149
; TYPE: PRT

; ORGANISM: Homo sapiens
US-10-408-765A-2270
Alignment Scores:
Pred. No.: 1.06e-65 Length: 149
Score: 764.00 Matches: 149
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 84.79% Indels: 0
DB: 16 Gaps: 0

US-10-649-952A-2 (1-501) x US-10-408-765A-2270 (1-149)
Qy 52 ATGAAGTGTGTAAGTCTTCAACGCCAGAGAGGTGAAGAGCGCAAGAGCGGTGCTC 111
Db 1 MetLysValArgLysSerSerThrProGluGluValLysLysArgLysLysAlaValLeu 20
Qy 112 TTCTGCCCTGAGTGAGGACAAAGAAACATCATCTCGAGGAGGCGCAAGAGATCTCGTG 171
Db 21 PheCysLeuSerGluAspLysLysAsnIleLeuGluGluGlyLysGluIleLeuVal 40
Qy 172 GGCATGTGGGCCAGACTGTGCGAGCATCCCTAGCCACCTTTGTCAAGATGCTGCCAGAT 231
Db 41 GlyAspValGlyGlnThrValAspAspProTyAlaThrPheValLysMetLeuProAsp 60
Qy 232 AAGGACTGCGCTATGCTCTATGATGCAACCTATGAGACCAAGAGAGCAAGAGGAG 291
Db 61 LysAspCysArgTyAlaLeuTyralaLeuTyralaLeuTyralaLeuTyralaLeu 80
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Db 101 AlaSerSerLysAspAlaIleLysLysLysLeuThrGlyIleLysHisGluLeuGlnAla 120
Qy 412 AACTGTCTACGAGAGGTCAAGGACCGCTGACCCCTGCGAGAGAGCTGGGGGCGAGTGC 471
Db 121 AsnCysTyralaLeuValLysAspArgCysThrLeuAlaGluLysLeuGlySerAla 140
Qy 472 GTCATCTCTCCCTGGAGGCGCAAGCCTTTG 498
Db 141 ValIleSerLeuGluGlyLysProLeu 149

RESULT 3
US-10-205-342-21
; Sequence 21, Application US/10205342
; Publication No. US20030108906A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert Company
; APPLICANT: Lee, Kevin
; APPLICANT: Dixon, Alistair
; APPLICANT: Brooksbank, Robert
; APPLICANT: Pinnock, Robert
; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
; FILE REFERENCE: WI-A-018198
; CURRENT APPLICATION NUMBER: US/10/205,342
; CURRENT FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: GB 0118354.0
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: Protein: Cofilin
US-10-205-342-21
Alignment Scores:
Pred. No.: 1.21e-59 Length: 166

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Score: 702.00 Matches: 135
Percent Similarity: 89.76% Conservative: 14
Best Local Similarity: 81.33% Mismatches: 17
Query Match: 77.91% Indels: 0
DB: 14 Gaps: 0

US-10-649-952A-2 (1-501) x US-10-205-342-21 (1-166)

QY 1 ATGGCTCCGGTGTGCTCTGATGTTCAAGGTGTTCAACGACATGAAGGTG 60
DB 1 MetAlaSerGlyValThrValAsnAspGluValLeuValPheAsnAspMetLeuVal 20
QY 61 CGTAAGTCTTCAAGCCAGAGGAGTCAAGAGCGCAAGAGCGGCTCTTCTGCGTG 120
DB 21 ArgLysSerSerThrGlnGluGluLeuLysArgLysLysAlaValLeuPheCysLeu 40
QY 121 AGTGAGGACAAAGAAACATCATCTCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180
DB 41 SerAspAspLysArgGlnIleValGluLysGlnIleValGluLysGlnIleValGlyAspIle 60
QY 181 GGCAGACTCTGACGATCCCTAGCCACCTTTGTCAAGATGCTGCCAGATAAGGACTGC 240
DB 61 GlyAspThrValGluAspProTyrThrSerPheValLysLeuLeuProLeuAsnAspCys 80
QY 241 CGTATGCTCTATGATGCAACCTATGACACCGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
DB 81 ArgTyrAlaLeuTyrAspAlaThrTyrGluThrLysGluSerLysLysGluAspLeuVal 100
QY 301 TTTATCTTCTGGCCCGGAGTCTGCGCCCTTAAGAGCAAAATGATTTATGCGAGCTCC 360
DB 101 PheLeuPheTrpAlaProGluSerAlaProLeuLysSerLysMetIleTyrAlaSerSer 120
QY 361 AAGGAGCCATCAAGAGAGCTGACAGGAGTCAAGGATCAAGTCAAGTCAAGTCAAGTCAAG 420
DB 121 LysAspAlaIleLysLysLysPheThrGlyLeuLysGlnTrpGlnValAsnGlyLeu 140
QY 421 GAGGAGTCAAGAGCCGCTGACCCCTGGCAGAGAGCTGGGGGCGAGTGGCGTCACTCC 480
DB 141 AspAspIleLysAspArgSerThrLeuGlyGluLysLeuGlyGlySerValValSer 160
QY 481 CTGAGGGCAAGCCTTTG 498
DB 161 LeuGluGlyLysProLeu 166

RESULT 4
US-10-649-952A-2
; Sequence 72, Application US/10205823
; Publication No. US20030108963A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gamavara, Manjula
; APPLICANT: Gorbacheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Monsey, Angela M.
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205,823
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746

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; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-205-823-72

Alignment Scores:
Pred. No.: 2,37e-59 Length: 166
Score: 699.00 Matches: 134
Percent Similarity: 89.76% Conservative: 15
Best Local Similarity: 80.72% Mismatches: 17
Query Match: 77.58% Indels: 0
DB: 14 Gaps: 0

US-10-649-952A-2 (1-501) x US-10-205-823-72 (1-166)

QY 1 ATGGCTCCGGTGTGCTCTGATGTTCAAGGTGTTCAACGACATGAAGGTG 60
DB 1 MetAlaSerGlyValThrValAsnAspGluValLeuValPheAsnAspMetLeuVal 20
QY 61 CGTAAGTCTTCAAGCCAGAGGAGTCAAGAGCGCAAGAGCGGCTCTTCTGCGTG 120
DB 21 ArgLysSerSerThrGlnGluGluLeuLysArgLysLysAlaValLeuPheCysLeu 40
QY 121 AGTGAGGACAAAGAAACATCATCTCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180
DB 41 SerAspAspLysArgGlnIleValGluLysGlnIleValGluLysGlnIleValGlyAspIle 60
QY 181 GGCAGACTCTGACGATCCCTAGCCACCTTTGTCAAGATGCTGCCAGATAAGGACTGC 240
DB 61 GlyAspThrValGluAspProTyrThrSerPheValLysLeuLeuProLeuAsnAspCys 80
QY 241 CGTATGCTCTATGATGCAACCTATGACACCGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
DB 81 ArgTyrAlaLeuTyrAspAlaThrTyrGluThrLysGluSerLysLysGluAspLeuVal 100
QY 301 TTTATCTTCTGGCCCGGAGTCTGCGCCCTTAAGAGCAAAATGATTTATGCGAGCTCC 360
DB 101 PheLeuPheTrpAlaProGluSerAlaProLeuLysSerLysMetIleTyrAlaSerSer 120
QY 361 AAGGAGCCATCAAGAGAGCTGACAGGAGTCAAGGATCAAGTCAAGTCAAGTCAAGTCAAG 420
DB 121 LysAspAlaIleLysLysLysPheThrGlyLeuLysGlnTrpGlnValAsnGlyLeu 140
QY 421 GAGGAGTCAAGAGCCGCTGACCCCTGGCAGAGAGCTGGGGGCGAGTGGCGTCACTCC 480
DB 141 AspAspIleLysAspArgSerThrLeuGlyGluLysLeuGlyGlySerValValSer 160
QY 481 CTGAGGGCAAGCCTTTG 498
DB 161 LeuGluGlyLysProLeu 166

RESULT 5
US-10-408-765A-1910
; Sequence 1910, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Wainock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A

```

```

; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 1910
; LENGTH: 166
; TYPE: PrT
; ORGANISM: Homo sapiens
US-10-408-765A-1910

```

Alignment Scores:		
Pred. No.:	2,378-59	Length:
Score:	699.00	Matches:
Percent Similarity:	89.7%	Conservative:
Best Local Similarity:	80.72%	Mismatches:
Query Match:	77.58%	Indels:
DB:	16	Gaps:
		0
		166
		134
		15
		0
		0

US-10-649-952A-2 (1-501) x US-10-408-765A-1910 (1-166)

QY	1	ATGGCCTCCGGTGTGGCTGTCTCTCTGATGGTGTCTCAAGGTGTTCAACGACATGAAGGTS	60
Db	1	MetAlaSerGlyValThrValAsnAspGluValIleLysValPheAsnAspMetLysVal	20
QY	61	CCTAAGTCTTCACGCCACGAGAGGTGAGAGCGCGAAGCGCGGTGCTCTCTCCCTG	120
Db	21	ArgLysSerSerThrGlnGluGluIleLysLysArgLysLysAlaValLeuPheCysLeu	40
QY	121	AGTGAGGACAAAGAGAATCATCTCTGGAGGAGGCGAGAGATCTGTGGCGCATGTG	180
Db	41	SerAspAspLysArgGlnIleValIleGluAlaLysGlnIleLeuValGlyAspIle	60
QY	181	GGCCAGACTGTCAGCATCCCTACGCCACCTTTGTCAAAGATGTCGCAGATAAGGACTGC	240
Db	61	GlyAspThrValGluAspProTyrThrSerPheValLysLeuLeuProLeuAsnAspCys	80
QY	241	CGCTATGCCCTCTATGATGCACCTATCAGACCAGAGAGACGAAGGAGGACTCTGGTG	300
Db	81	ArgTyrAlaLeuTyrAspAlaThrTyrGluThrLysGluSerLysLysGluAspLeuVal	100
QY	301	TTTATCTTCTGGGCCCCGAGCTGCGCCCTTAAGAGCAAAATGATTATGCCAGCTCC	360
Db	101	PheIlePheTrpAlaProGluSerAlaProLeuLysSerLysMetIleTyrAlaSerSer	120
QY	361	RAGGACGCCATCAAGAAGACTCAGAGGATCAAGCATCAATTGCAAGCAACTGCTAC	420
Db	121	LysAspAlaIleLysLysPheThrGlyIleLysHisGluTrpGlnValAsnGlyLeu	140
QY	421	GAGGAGGTCAAAGGACCGCTGCACCTCGCGACAGAAAGCTGGGGCGCATGCGGTCACTCC	480
Db	141	AspAspIleLysAspArgSerThrLeuGlyGluLysLeuGlyAsnValValSer	160
QY	481	CTGGAGGCAAGCCCTTTG	498
Db	161	LeuGluGlyLysProLeu	166

RESULT 6

```

US-10-158-034-93
; Sequence 93, Application US/10158034
; Publication No. US20030219758A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ10C1
; CURRENT APPLICATION NUMBER: US/10/158,034
; CURRENT FILING DATE: 2002-05-31
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 93
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-158-034-93

```

Alignment Scores:	
Pred. No.:	2,49e-59
Score:	699.00
Percent Similarity:	89.76%
Best Local Similarity:	80.72%
Query Match:	77.58%
DB:	15
Length:	205
Matches:	134
Conservative:	15
Mismatches:	17
Indels:	0
Gaps:	0

US-10-649-952A-2 (1-501) x US-10-158-034-93 (1-205)

QY	1	ATFGCGCTCCGGTGGCTGCTCTCTGATGGTGCATCAAGGTGTTCACACGACATGAAGGTG	60
Db	40	MetAlaSerGlyValThrValAsnAspGluValIleLysValPheAsnAspMetLysVal	59
QY	61	CGTAACTCTTCAACGCCACGAGGAGGTCAAGACGGCAAGACGGGTGCTCTCTCCCTG	120
Db	60	ArgLysSerSerThrGlnGluGluIleLysLysArgLysLysAlaValLeuPheCysLeu	79
QY	121	ACTGAGGACAAAGAACATCATCTCTGAGGAGGGCAAGGAGATCCTGGTGGCGCATGTG	180
Db	80	SerAspLysArgGlnIleValGluLysGlnIleLeuValGlyAspIle	99
QY	181	GGCCAGACTGCGACGATCCCTACGCCACCTTTGTCAAGATGTCGCAGATAAGGACTCC	240
Db	100	GlyAspThrValGluAspProTyrThrSerPheValLysLeuLeuProLeuAsnAspCys	119
QY	241	CGCTATGGCCTCTATGATGCACCTATGAGACCAAGAGAGAGAGAGATCTGGTG	300
Db	120	ArgTyrAlaLeuTyrAspAlaThrTyrGluThrLysGluSerLysLysGluAspLeuVal	139
QY	301	TTTATCTTCCTGGGCCCGGAGTCTGCGCCCTTAAGAGCAAAATGATTATGCCAGCTCC	360
Db	140	PheIlePheTrpAlaProGluSerAlaProLeuLysSerLysMetIleTyrAlaSerSer	159
QY	361	AAGGACGCCATCAAGAAGAAGCTCACAGGATCAAGCATGAATTGCAAGCAAACTGCTAC	420
Db	160	LysAspAlaIleLysLysLysPheThrGlyIleLysHisGluTrpGlnValIleGlyLeu	179
QY	421	GAGGAGGTCAAGGACCGCTGCACCCTGGCAGAGAGCTGGGGGGCAGTCGGTCTCC	480
Db	180	AspAspIleLysAspArgSerThrLeuGlyGluLysLeuGlyGlyAsnValValValSer	199
QY	481	CTGGAGGCGAAGCCCTTTC	498
Db	200	LeuGluGlyLysProLeu	205

RESULT 7

```

US-10-408-765A-2351
; Sequence 2351, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fany, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2351
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-2351
Alignment Scores:

```


Pred. No.: 1 45e-45 Length: 148
Score: 557.50 Matches: 108
Percent Similarity: 84.56% Conservative: 18
Best Local Similarity: 72.48% Mismatches: 22
Query Match: 61.88% Indels: 1
DB: 16 Gaps: 1

US-10-649-952A-2 (1-501) x US-10-408-765A-2351 (1-148)

QY 52 ATGAAGTGGTGAAGTCTTCAACGCCAGAGAGGTGAAGAGCGCGGTGCTC 111
Db 1 MetLysValArgLysCysSerThrProGluIleLysLysArgLysLysAlaValIle 20
QY 112 TTCTGCTGAGTGAAGCAAGAGAACATCTCTGGAGAGGCGCAAGAGATCCTGGTG 171
Db 21 PheCysLeuSerAlaAspLysLysCysIleValGluGluGlyLysGluIleLeuVal 40
QY 172 GCGAGTGTGGCCAGAGTGCAGAGTCCCTAGCCACCTTCTCAAGATGCTGCCAGAT 231
Db 41 GlyAspValGlyValThrIleThrAspPropHelyHisPheValGlyMetLeuProGlu 60
QY 232 AAGGACTCGCGCTATGCTCTATGATCAACCTATGAGACCAAGAGAGCAAGAGAG 291
Db 61 LysAspCysArgTyrAlaLeuTyrAspAlaSerPheGluThrLysGluSerArgLysGlu 80
QY 292 GATCTGTGTTATCTTCTGGCGCCCGAGTCTGCGCCCTTAAAGAGCAAAATGATTAT 351
Db 81 GluLeuMetPhePheLeuTyrAlaProGluLeuAlaProLeuLysSerLysMetIleTyr 100
QY 352 GCAGCTCCAGAGCGCCATCAAGAGAGCTACAGAGGATCAAGATGATGCAAGCA 411
Db 101 AlaSerSerLysAspAlaIleLysLysLysPheGlnGlyIleLysHisGluCysGlnAla 120
QY 412 AACTGTACAGAGAGTCAAGAGCGCTGCACCTGCAGAGAGCTGGGGGCGAGTGGC 471
Db 121 AsnGlyProGluAspLeuAsnArgAlaCys---IleAlaGluLysLeuGlySerLeu 139
QY 472 GTCATCTCCCTGGAGGCGCAAGCCTTTG 498
Db 140 IleValAlaPheGluGlyCysProVal 148

RESULT 8

US-10-158-034-94
; Sequence 94, Application US/10158034
; Publication No. US20030219758A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ10C1
; CURRENT APPLICATION NUMBER: US/10/158,034
; CURRENT FILING DATE: 2002-05-31
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 94
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (107)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (123)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (126)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (127)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (128)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-158-034-94

Alignment Scores:

Pred. No.: 4 53e-36 Length: 129
Score: 460.00 Matches: 87
Percent Similarity: 90.65% Conservative: 10
Best Local Similarity: 81.31% Mismatches: 10
Query Match: 51.05% Indels: 0
DB: 15 Gaps: 0

US-10-649-952A-2 (1-501) x US-10-158-034-94 (1-129)

QY 1 ATGGCCTCGGTGGTGGCTCTCTGATGTCATCAAGGTGTTCAACGACATGAAGGTG 60
Db 13 MetAlaSerGlyValThrValAsnAspGluValIleLysValPheAsnAspMetLysVal 32
QY 61 CGTAAGTCTTCAACGCCAGAGAGGTGAAGAGCGCAAGAGCGGTGCTCTTCTCCCTG 120
Db 33 ArgLysSerSerThrGlnGluLysLysLysArgLysLysAlaValLeuPheCysLeu 52
QY 121 AGTGAGCAAGAGAACATCATCTCTGGAGAGGCGCAAGAGAGATCTGTGGCGGATGTG 180
Db 53 SerAspAspLysArgGlnIleValGluGluAlaLysGlnIleLeuValGlyAspIle 72
QY 181 GCCAGACTGTGCGAGATCCCTACGCCCTTTGTCAAGATCTGCCAGATAAGGACTGC 240
Db 73 GlyAspThrValGluAspProTyrThrSerPheValLysLeuLeuProLeuAsnAspCys 92
QY 241 CGCTATGCCCTCTATGATCAACCTATGAGACCAAGAGAGCAAGAGAGATCTGGTG 300
Db 93 ArgTyrAlaLeuTyrAspAlaThrTyrGluThrLysGluSer***LysGluAspLeuVal 112
QY 301 TTTATCTTCTGGCGCCCGAG 321
Db 113 PheIlePheTrpAlaProGlu 119

Alignment Scores:

Pred. No.: 4 48e-35 Length: 156
Score: 450.00 Matches: 85
Percent Similarity: 91.35% Conservative: 10
Best Local Similarity: 81.73% Mismatches: 9
Query Match: 49.94% Indels: 0
DB: 15 Gaps: 0

US-10-649-952A-2 (1-501) x US-10-158-034-68 (1-156)

QY 1 ATGGCCTCGGTGGTGGCTCTCTGATGTCATCAAGGTGTTCAACGACATGAAGGTG 60
Db 45 MetAlaSerGlyValThrValAsnAspGluValIleLysValPheAsnAspMetLysVal 64

QY 61 CGTAAGTCTTCAAGCCAGAGAGGTGAAGAAGCGCAAGAGCGGTCTTCTGCTG 120
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 65 ArglySerSerThrGlnGluLeuIleValGlySerGlySerGlySerGlySerGlySer 84
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 QY 121 AGTGAGGACAAAGAACATCATCTCTGAGGAGGCGCAAGAGATCTCTGGGCGATGTG 180
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 85 SerAspAspLysArgGlnIleValGluGluAlaLysGlnIleValGlyAspIle 104
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 QY 181 GGCAGAGCTGCGAGATCCCTAGCCACCTTCTCAAGATGCTGCCAGATAAGGACTGC 240
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 105 GlyAspThrValGluAspProTyrThrSerPheValLysLeuLeuProLeuAsnAspCys 124
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 QY 241 CGCTATGCGCTCTATGATCAACCTATGAGACCAAGAGAGCAAGAGGAGATCTGGTG 300
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 125 ArgTyrAlaLeuTyrAspAlaThrTyrGluThrLysGluSerLysLysGluAspLeuVal 144
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 QY 301 TTTATCTCTGG 312
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 145 PheIlePheTrp 148
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 10

US-10-264-049-4340
 ; Sequence 4340, Application US/10264049
 ; Publication No. US20040005579A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Birse et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: P4133P1
 ; CURRENT APPLICATION NUMBER: US/10/264,049
 ; CURRENT FILING DATE: 2002-10-04
 ; PRIOR APPLICATION NUMBER: PCT/US01/18569
 ; PRIOR FILING DATE: 2001-06-07
 ; PRIOR APPLICATION NUMBER: US 60/209,467
 ; PRIOR FILING DATE: 2000-06-07
 ; NUMBER OF SEQ ID NOS: 4360
 ; SOFTWARE: PatentIn Ver. 3.1
 ; SEQ ID NO 4340
 ; LENGTH: 106
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: MISC FEATURE
 ; LOCATION: (91)-
 ; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
 ; FEATURE:
 ; NAME/KEY: MISC FEATURE
 ; LOCATION: (100)
 ; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
 US-10-264-049-4340

Alignment Scores:
 Pred. No.: 7,46e-18 Length: 106
 Score: 273.00 Matches: 58
 Percent Similarity: 67.62% Conservative: 13
 Best Local Similarity: 55.24% Mismatches: 34
 Query Match: 30.30% Indels: 0
 DB: 15 Gaps: 0

US-10-649-952A-2 (1-501) x US-10-264-049-4340 (1-106)

QY 22 TCTGATGGTGTCATCAAGGTCTTCAACGACATGAAGTGGCTAAGTCTTCAAGCCGAG 81
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 1 AlaAspGluValCysArgGlyPheTyrAspMetLysValArgLysCysSerThrProGlu 20
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 QY 82 GAGGTGAAGAGCGCAAGAGCGGTGCTCTTCTGCTGAGTGAGGACAAAGAACATC 141
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 21 GluIleLysLysArgLysLysAlaValIlePheCysLeuSerAlaAspLysLysCysIle 40
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 QY 142 ATCTGAGGAGGCGCAGGAGATCTGTGGGCGATGTGGGCGAGACTGTGAGCATCCC 201
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 41 IleValGluGluGlyLysGluIleValGlyAspValGlyValThrIleThrAspPro 60
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 202 TACGCCACCTTTGTCAAGATGCTGCCAGATAAGGACTGCCGCTATATGATGCA 261
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 61 PheIleHisPheValGlyMetLeuLeuLysLysIleValAlaMetLeuCysMetMetGln 80
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 QY 262 ACCTATGAGACCAAGGAGAGCAAGAGGAGATCTGTGTTTATCTTCTGGGCCCCGAG 321
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 81 AlaLeuLysGlnLysAsnSerGluLysLys***LeuMetPhePheTrpGlyAlaPro*** 100
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 QY 322 TCTGGCGCCCTTAAAG 336
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 101 LeuGlyThrPheLys 105
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 11

US-10-369-493-22293
 ; Sequence 22293, Application US/10369493
 ; Publication No. US20030233675A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Chen, Xianfeng
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 ; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
 ; FILE REFERENCE: 38-10(52052)B
 ; CURRENT APPLICATION NUMBER: US/10/369,493
 ; CURRENT FILING DATE: 2003-02-28
 ; PRIOR APPLICATION NUMBER: US 60/360,039
 ; PRIOR FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 47374
 ; SEQ ID NO 22293
 ; LENGTH: 143
 ; TYPE: PRT
 ; ORGANISM: Saccharomyces cerevisiae
 US-10-369-493-22293

Alignment Scores:
 Pred. No.: 2,76e-17 Length: 143
 Score: 267.50 Matches: 54
 Percent Similarity: 59.44% Conservative: 31
 Best Local Similarity: 29.76% Mismatches: 37
 Query Match: 27.69% Indels: 21
 DB: 15 Gaps: 3

US-10-649-952A-2 (1-501) x US-10-369-493-22293 (1-143)

QY 7 TCCGGTGTGCTGTCTCTGATGTGTATCAAGGTGTTCAACGACATGAAGTCCGTAAG 66
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 4 SerGlyValAlaValAlaAspGluSerLeuThrAlaPheAsnAspLeuLys----- 20
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 QY 67 TCTTCAAGCCAGAGGAGGTGAAGAGCGGCAAGAGCGGTGCTCTTCTGCCTGAGTGAG 126
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 21 -----LeuGlyLysLysTyrLysPheIleLeuPheGlyLeuAsnAsp 34
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 QY 127 GACAAGAAGAACATCATCTCGAGAGCGGCAAGAGAGATCCTGTGGGCGATGTGGGCCAG 186
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 35 AlaLysThrGluIleValValLysGlu-----Thr 44
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 QY 187 ACTGTGACGATCCCTACGCCACCTTTGTCAAGATGTCGACATAGAGACTGCCGCTAT 246
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 45 SerThrAspProSerTyrAspAlaPheLeuLysLeuProGluAsnAspCysLeuTyr 64
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 QY 247 GCCTCTATGATCAACCTATGAGACC-----AAGGAGACGAGAGGAGGATCTGGTG 300
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 65 AlaIleTyrAspPheGluTyrGluIleAsnGlyAsnGlyLysArgSerLysIleVal 84
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 QY 301 TTTATCTTCTGGGCCCCGAGTCTGCCCTTAAAGACAAATGATTTATGCCAGTCC 360
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 85 PhePheThrTrpSerProAspThrAlaProValArgSerLysMetValTyrAlaSerSer 104
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 QY 361 AAGACGCCATCAAGAGAGCTGACAGGATCAAGCATGAATTCAGCAAACTGCTAC 420
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 105 LysAspAlaLeuArgArgAlaLeuAsnGlyValSerThrAspValGlnGlyThrAspPhe 124
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```
QY 421 GAGGAGTC 429
Db 125 SerGluVal 127

RESULT 12
US-10-263-255-2
; Sequence 2, Application US/10263255
; Publication NO. US20040191771A1
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; APPLICANT: Chua, Penelope
; APPLICANT: Nislow, Corey
; TITLE OF INVENTION: Candida Albicans Cofilin
; FILE REFERENCE: CYTOP072
; CURRENT APPLICATION NUMBER: US/10/263,255
; CURRENT FILING DATE: 2002-10-01
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Candida Albicans
US-10-263-255-2

Alignment Scores:
Pred. No.: 6,37e-16 Length: 141
Score: 253.50 Matches: 48
Percent Similarity: 60.14% Conservative: 38
Best Local Similarity: 33.57% Mismatches: 36
Query Match: 28.14% Indels: 21
DB: 16 Gaps: 3

US-10-649-952A-2 (1-501) x US-10-263-255-2 (1-141)
QY 7 TCCGGTGTGGCTGCTCTGATGTCATCAAGGTCTTCAACGACATGAAGTGCCTAAG 66
Db 4 SerGlyValThrValAlaAspGluSerLeuThrAlaPheAsnAspLeuLys----- 20
QY 67 TCTTCAACGCCAGAGGAGGTGAAGAGCGCAAGCGGTCTCTTCTGCTGAGTGAG 126
Db 21 -----LeuGlyArgLysTyrLysPheValIlePheProLeuAsnAsp 34
QY 127 GACAAGAAACATCATCTCGGAGGAGGCGCAAGGAGATCCTGGTGGCGATGTGGCCAG 186
Db 35 GluLysThrGlnIleValGluGln-----Thr 44
QY 187 ACTGTGACGATCCCTACGCCACCTTTGTCAAGATCTGCCAGATAAGACTGCCCTAT 246
Db 45 SerThrGluGlnGluTyrAspAlaPheLeuGluLysLeuProGluAsnGluCysArgTyr 64
QY 247 GCCTCTATGATCAACCTATGAGACC-----AAGGAGAGCAAGAGGAGTCTGGTG 300
Db 65 AlaValTyrAspPheGluTyrAspIleGlyGlyGluLysArgSerLysIleVal 84
QY 301 TTTATCTTCTGGCCCCCGAGTCTGCGCCCTTTAAGAGCAAAATGATTTATGCGACTCC 360
Db 85 PhePheThrTrpSerProAspThrAlaProValArgAlaLysMetValTyrAlaSerSer 104
QY 361 AAGGAGCCCATCAAGAAAGCTGACAGGATCAAGCATGAATTGCAAGCAAACTGCTAC 420
Db 105 LysAspSerLeuArgAlaLeuAsnGlyValAlaAlaAspValGlnGlyThrAspPhe 124
QY 421 GAGGAGTC 429
Db 125 SerGluVal 127

RESULT 13
US-10-263-255-4
; Sequence 4, Application US/10263255
; Publication NO. US20040191771A1
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
```

```
; APPLICANT: Chua, Penelope
; APPLICANT: Nislow, Corey
; TITLE OF INVENTION: Candida Albicans Cofilin
; FILE REFERENCE: CYTOP072
; CURRENT APPLICATION NUMBER: US/10/263,255
; CURRENT FILING DATE: 2002-10-01
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Candida albicans
US-10-263-255-4

Alignment Scores:
Pred. No.: 3,84e-15 Length: 141
Score: 245.50 Matches: 48
Percent Similarity: 59.44% Conservative: 37
Best Local Similarity: 33.57% Mismatches: 37
Query Match: 27.25% Indels: 21
DB: 16 Gaps: 3

US-10-649-952A-2 (1-501) x US-10-263-255-4 (1-141)
QY 7 TCCGGTGTGGCTGCTCTGATGTCATCAAGGTCTTCAACGACATGAAGTGCCTAAG 66
Db 4 SerGlyValThrValAlaAspGluSerLeuThrAlaPheAsnAspLeuLys----- 20
QY 67 TCTTCAACGCCAGAGGAGGTGAAGAGCGCAAGCGGTCTCTTCTGCTGAGTGAG 126
Db 21 -----LeuGlyArgLysTyrLysPheValIlePheProLeuAsnAsp 34
QY 127 GACAAGAAACATCATCTCGGAGGAGGCGCAAGGAGATCCTGGTGGCGATGTGGCCAG 186
Db 35 GluLysThrGlnIleValGluGln-----Thr 44
QY 187 ACTGTGACGATCCCTACGCCACCTTTGTCAAGATCTGCCAGATAAGACTGCCCTAT 246
Db 45 SerThrGluGlnGluTyrAspAlaPheLeuGluLysLeuProGluAsnGluCysArgTyr 64
QY 247 GCCTCTATGATCAACCTATGAGACC-----AAGGAGAGCAAGAGGAGTCTGGTG 300
Db 65 AlaValTyrAspPheGluTyrAspIleGlyGlyGluLysArgSerLysIleVal 84
QY 301 TTTATCTTCTGGCCCCCGAGTCTGCGCCCTTTAAGAGCAAAATGATTTATGCGACTCC 360
Db 85 PhePheThrTrpSerProAspThrAlaProValArgAlaLysMetValTyrAlaSerSer 104
QY 361 AAGGAGCCCATCAAGAAAGCTGACAGGATCAAGCATGAATTGCAAGCAAACTGCTAC 420
Db 105 LysAspSerLeuArgAlaLeuAsnGlyValAlaAlaAspValGlnGlyThrAspPhe 124
QY 421 GAGGAGTC 429
Db 125 PheGluVal 127

RESULT 14
US-10-424-599-186070
; Sequence 186070, Application US/10424599
; Publication NO. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 186070
; LENGTH: 139
```

```
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_139033C.1.pep
US-10-424-599-186070

Alignment Scores:
Pred. No.: 1.47e-14 Length: 139
Score: 239.50 Matches: 52
Percent Similarity: 53.02% Conservative: 27
Best Local Similarity: 34.90% Mismatches: 51
Query Match: 26.58% Indels: 19
DB: 15 Gaps: 3

US-10-649-952A-2 (1-501) x US-10-424-599-186070 (1-139)
Qy 7 TCCGGTGGCTGCTCTGTGATGTCATCAGAGTTCATCAGACATCAAGTGGGTGAAG 66
Db :::::::::::::::::::::
Qy 4 ThrGlyTleAlaValAspAsnGluCysValAsnGluPheAsnAlaPheLysLeuArgAsn 23
Db :::::::::::::::::::::
Qy 67 TCTTCAACGCCAGAGGAGGTGAAGAAGCGCAAGAGCGGTCTCTTCTGCTCGCTGAGT 126
Db :::::::::::::::::::::
Qy 24 Thr-----HisArgTyrIleValPhe----- 30
Db :::::::::::::::::::::
Qy 127 GACAAGAAGACATCATCTCGAGAGGCGCAAGAGATCTCTGTGGCGCATGTGGCCAG 186
Db :::::::::::::::::::::
Qy 31 -----LysIleGluAsnAlaLysGluIleLysIleGluLysGlyGlu 45
Db :::::::::::::::::::::
Qy 187 ACTGTGAGAGTCCCTGACGCCACCTTCTCAGATGTCGCCAGATAAGACTGCCGTAT 246
Db :::::::::::::::::::::
Qy 46 ThrThrAlaSer---TyrAspGluPheLeuLysGlnLeuProAspAsnAspCysArgTyr 64
Db :::::::::::::::::::::
Qy 247 GCCCTCTATGATCAACCTATGAGACCAAGAGAGGAGGAGGATCTGCTGTTATC 305
Db :::::::::::::::::::::
Qy 65 AlaValTyrAsnGluTyrAsnGlnAlaAspGlyPheArgSerLysIleValPhePhe 84
Db :::::::::::::::::::::
Qy 307 TTCTGGGCCCCGAGTCTGCGCCCTTAAGAGCAAAATGATTATGCCAGCTCCAAGGAC 366
Db :::::::::::::::::::::
Qy 85 LeuTrpAlaProAspThrAlaProThrLysSerLysMetLeuTyrAlaGlyThrLysAsp 104
Db :::::::::::::::::::::
Qy 367 GCCATCAGAGAGCTGACAGGATCAAGCATGAATTGCAAGCAAACTGCTACGAGGAG 426
Db :::::::::::::::::::::
Qy 105 ThrLeuLysLysAsnLeuGlnGlyLeuGlnValGluMetGlnGlyThrAspLysSerGlu 124
Db :::::::::::::::::::::
Qy 427 GTCAGGAGCCGTCGACCCCTGCAGAG 453
Db :::::::::::::::::::::
Qy 125 ValAspGlnSerGluValLeuAlaLys 133

RESULT 15
US-10-029-386-30107
; Sequence 30107, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; FILE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AECOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 30107
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL132765.16
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.3
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.6
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 9.9
; OTHER INFORMATION: SWISSPROT HIT: P18282, EVALUATE 1.00e-29

US-10-029-386-30107
Alignment Scores:
Pred. No.: 1.02e-13 Length: 60
Score: 230.00 Matches: 43
Percent Similarity: 89.66% Conservative: 9
Best Local Similarity: 74.14% Mismatches: 6
Query Match: 25.53% Indels: 0
DB: 14 Gaps: 0

US-10-649-952A-2 (1-501) x US-10-029-386-30107 (1-60)
Qy 130 AAGAAGAACATCATCTCTGGAGGAGGCAAGAGATCTGTGGCGATGTGGCGCAGACT 189
Db :::::::::::::::::::::
Qy 1 LysLysCysIleIleValGluGluGlyLysGluIleLeuValGlyAspValGlyValThr 20
Db :::::::::::::::::::::
Qy 190 GTCAGCATCCCTACGCCACCTTTGTCAAGATGTCAGATAGGACTGCCGCTATGCC 249
Db :::::::::::::::::::::
Qy 21 IleThrAspProPheLysHisPheValGlyMetLeuProGluLysAspCysArgTyrAla 40
Db :::::::::::::::::::::
Qy 250 CTCTATGATCAACCTATGAGACCAAGAGAGCAAGAGGAGGATCTGGTGTGTTT 303
Db :::::::::::::::::::::
Qy 41 LeuTyrAspAlaSerPheGluThrLysGluSerArgLysGluGluLeuMetPhe 58
Db :::::::::::::::::::::

Search completed: May 13, 2005, 10:05:21
Job time : 108.5 secs
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